

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:34:20 ; Search time 91.4571 Seconds
(without alignments)
558.211 Million cell updates/sec

Title: US-09-706-325-24

Perfect score: 132

Sequence: 1 SYMTINNFSCREEMGEVI.....EANGLLPDKLTLFCEVSVV 132

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_16Dec04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	132	4	Aae03669 Human SPO
2	132	100.0	180	4	Aae03662 Human SPO
3	132	100.0	374	4	Abb90799 Human she
4	132	100.0	374	4	Aae03659 Human SPO
5	132	100.0	374	7	Abb85287 Human pro
6	132	100.0	374	7	Adi62718 Human apo
7	132	100.0	374	8	Adg89936 Antagonis
8	132	100.0	374	8	Adg89928 Antagonis
9	132	100.0	385	3	Abb58286 Lung canc
10	63	47.7	398	4	Abg23713 Novel hum
11	53	40.2	391	4	Abb94987 Human pro
12	53	40.2	391	8	Adg89926 Antagonis
13	53	40.2	391	8	Adg89934 Antagonis
14	53	40.2	392	5	Abp43818 FLJ11857
15	53	40.2	392	6	Abp43818 FLJ11857
16	40	30.3	377	4	Abb64759 Drosophil
17	40	30.3	377	8	Abb64759 Drosophil
18	35	26.5	35	4	Abb40093 Peptide #
19	35	26.5	35	4	Aam33727 Peptide #
20	35	26.5	35	4	Aam73533 Human bon
21	35	26.5	35	4	Aam60850 Human bra
22	35	26.5	35	4	Abg55260 Human liv
23	35	26.5	35	5	Abg43394 Human pep
24	33	25.0	195	4	Aau16237 Human nov
25	33	25.0	195	6	Abu55306 Human nov

Abb84635 S. aureus
Adf09194 S. aureus
Adh39727 Streptomy
Aam87295 Human lmm
Adf59258 Human pol
Abu11487 Human MDD
Abu11676 Human MDD
Aag12069 Arabidops
Aag12068 Arabidops
Aag15516 Arabidops
Aag27321 B. napus
Aab27319 B. napus
Aab27320 B. napus
Aag54812 Human pro
Aag54811 Arabidops
Adb89576 Human pol
Adb39486 Protein e
Adal3323 Human int
Adb75613 Prostate
Adp45515 Human col
Aaw60983 Streptoco
Adh87756 Enterococ
Aab56508 Human pro
Ade54341 Rat Prote
Ade54337 Rat Prote
Ade54349 Rat Prote
Ade54345 Rat Prote
Aab87741 Human T2R
Aam40252 Human pol
Ade61720 Rat Prote
Ade61722 Human pro
Adk67697 Human Rab
Aam42038 Human pol
Abg19562 Novel hum
Abu45936 Protein e
Adk48740 Streptoco
Adr95625 Novel S.
Adf50364 Oil-assoc
Ado61905 Transcrip
Adn21114 Bacteri
Aab32256 HLA A0201
Aau68938 Human TAD
Adh13255 Human HLA
Adh78475 Human TAD
Aar21620 Sequence
Abg78461 Asparagin
Aar24891 Sequence
Adn197804 Sweet pot
Adn37732 Sweet pot
Adg59276 OGT relat
Aaw85067 Signal pe
Abb77593 Human can
Adn37752 Sweet pot
Aar55847 Human GCP
Aab49188 Lowest en
Aar55846 Human GCP
Aab30617 Streptoco
Abp30617 Streptoco
Abc59000 Human gen
Aar55845 Human GCP
Aar55849 Human GCP
Abb84647 Sweet pot
Adn37747 Sporamin
Aar74137 Potato sp

99	6	4.5	40	4	ABG54878	Abg54878 Human liv	172	6	4.5	98	4	AAU68923	Aau68923 Human SRC
100	6	4.5	41	5	ABG433008	Abg433008 Human pep	173	6	4.5	98	7	ADE13243	Ade13243 Scavenger
101	6	4.5	40	8	ADN37754	Adn37754 Sweet pot	174	6	4.5	98	8	ADH78452	Adh78452 Human TAD
102	6	4.5	42	2	AAI14007	Aai14007 Dnrk repe	175	6	4.5	99	4	AAO07330	Aao07330 Human pol
103	6	4.5	42	6	ADR83840	Adr83840 Escherich	176	6	4.5	100	2	AAI34819	Aai34819 Amino aci
104	6	4.5	42	7	ADF69983	Adf69983 AcMA-type	177	6	4.5	100	4	AAO00134	Aao00134 Human pol
105	6	4.5	42	7	ADP69979	Adp69979 AcMA-type	178	6	4.5	101	3	AAI54719	Aai54719 Arabidops
106	6	4.5	44	3	AB16864	Ab16864 Bacteriop	179	6	4.5	101	3	AAI24855	Aai24855 Human DED
107	6	4.5	45	4	ABE58480	Abb58480 Drosophil	180	6	4.5	101	5	AAE38898	Aae38898 Human DED
108	6	4.5	45	6	ABO14013	Abol14013 Novel hum	181	6	4.5	105	4	AAE07089	Aae07089 Human gen
109	6	4.5	45	8	ADN60710	Adn60710 Human sec	182	6	4.5	105	4	AAE07060	Aae07060 Human gen
110	6	4.5	46	2	AAI27608	Aai27608 Human sec	183	6	4.5	105	5	ABG65075	Abg65075 Human alb
111	6	4.5	46	6	ABU07202	Abu07202 Maize SSI	184	6	4.5	105	5	ABG65074	Abg65074 Human alb
112	6	4.5	46	8	ADG78419	Adg78419 Human sec	185	6	4.5	105	7	ABO72127	AbO72127 Pseudomon
113	6	4.5	50	7	ADE80757	Ade80757 Microsate	186	6	4.5	105	8	ADL78342	Adl78342 Albumin f
114	6	4.5	52	4	AAU57922	Aau57922 Propionib	187	6	4.5	105	8	ADL78341	Adl78341 Albumin f
115	6	4.5	52	6	ABM54441	Abm54441 Propionib	188	6	4.5	107	6	ABP76286	Abp76286 Human GEN
116	6	4.5	54	4	ABG14793	Abg14793 Novel hum	189	6	4.5	108	4	AAI91184	Aai91184 C glutami
117	6	4.5	57	4	AAU46439	Aau46439 Propionib	190	6	4.5	110	6	ABR39780	AbR39780 R. glutin
118	6	4.5	57	6	ABM42958	Abm42958 Propionib	191	6	4.5	110	7	ADC96062	Adc96062 E. faeciu
119	6	4.5	59	3	AAI12300	Aai12300 Zea mays	192	6	4.5	110	8	ADR10082	Adr10082 Human pro
120	6	4.5	62	5	ABP39591	Abp39591 Staphyloc	193	6	4.5	111	3	AAI7518	Aai7518 Arabidops
121	6	4.5	62	8	ADS05582	AdS05582 Staphyloc	194	6	4.5	111	4	ABBI0692	Abbi0692 Human pan
122	6	4.5	63	4	ABM84352	Abm84352 Human imm	195	6	4.5	111	4	AAI92990	Aai92990 Human dig
123	6	4.5	64	7	ADC97533	Adc97533 E. faeciu	196	6	4.5	111	4	AAE07115	Aae07115 Human gen
124	6	4.5	67	3	ABM56427	Abm56427 Human pro	197	6	4.5	112	3	AAI84445	Aai84445 Amino aci
125	6	4.5	67	8	ADJ67567	Adj67567 Human ova	198	6	4.5	112	3	AAI22299	Aai22299 Zea mays
126	6	4.5	67	8	ABO57060	AbO57060 Human gen	199	6	4.5	112	3	AAI45000	Aai45000 Zea mays
127	6	4.5	68	5	ABP39931	Abp39931 Staphyloc	200	6	4.5	112	3	AAI18819	Aai18819 Zea mays
128	6	4.5	69	5	ABP11387	Abp11387 Human ORF	201	6	4.5	112	6	ABJ25997	Abj25997 Aspergill
129	6	4.5	69	7	ADH35531	Adh35531 Partial s	202	6	4.5	113	2	AAI36449	Aai36449 Human che
130	6	4.5	73	4	AAO12563	Aao12563 Human pol	203	6	4.5	113	5	ABY78092	AbY78092 Amino aci
131	6	4.5	75	2	AAI55843	Aai55843 Human GCP	204	6	4.5	113	6	ABG73739	Abg73739 Human Cka
132	6	4.5	75	2	AAW96720	Aaw96720 Granulocy	205	6	4.5	114	2	AAW46286	Aaw46286 Human gra
133	6	4.5	75	6	ABU67722	Abu67722 Human CXC	206	6	4.5	114	5	AAU98084	Aau98084 Human SCY
134	6	4.5	75	6	ABU67722	Abu67722 Human CXC	207	6	4.5	114	6	ABU56721	Abu56721 Lung canc
135	6	4.5	75	7	ABE08089	AbE08089 GCP-2 che	208	6	4.5	114	6	ABJ25397	Abj25397 Aspergill
136	6	4.5	76	8	ADJ67568	Adj67568 Human ova	209	6	4.5	114	7	ABR44247	AbR44247 Human wil
137	6	4.5	77	3	AAI69024	Aai69024 Amino aci	210	6	4.5	114	7	ADE08120	Ade08120 Novel pro
138	6	4.5	77	3	AAI69024	Aai69024 Amino aci	211	6	4.5	114	7	ADF90874	Adf90874 Human hep
139	6	4.5	77	5	AAO20029	Aao20029 Human che	212	6	4.5	114	7	ADN39146	Adn39146 Cancer/an
140	6	4.5	77	5	AAO14162	Aao14162 Human GCP	213	6	4.5	114	7	ADN39996	Adn39996 Cancer/an
141	6	4.5	77	5	ADH32782	Adh32782 Yeast smo	214	6	4.5	114	8	ADQ76206	Adq76206 Chemokine
142	6	4.5	77	8	ADR90680	Adr90680 Human gra	215	6	4.5	115	3	AAI00876	Aai00876 Human sec
143	6	4.5	79	4	ABG12182	Abg12182 Novel hum	216	6	4.5	115	7	ABR44248	AbR44248 Human gra
144	6	4.5	80	4	AAI19769	Aai19769 Peptide #	217	6	4.5	115	7	ADF07301	Adf07301 Bacterial
145	6	4.5	80	4	ABB39569	Abb39569 Peptide #	218	6	4.5	115	7	ADH86054	Adh86054 Enterococ
146	6	4.5	80	4	AAI33128	Aai33128 Peptide #	219	6	4.5	117	3	AAI46694	Aai46694 Arabidops
147	6	4.5	80	4	AAI81490	Aai81490 Human hae	220	6	4.5	117	4	ABB67424	Abb67424 Drosophil
148	6	4.5	80	4	ABB24287	Abb24287 Protein #	221	6	4.5	117	5	ABP06380	Abp06380 Human ORF
149	6	4.5	80	4	AAI72897	Aai72897 Human bon	222	6	4.5	118	3	AAI5934	Aai5934 Arabidops
150	6	4.5	80	4	AAI60268	Aai60268 Human bra	223	6	4.5	118	4	ABG09835	Abg09835 Novel hum
151	6	4.5	80	4	ABG54605	Abg54605 Human liv	224	6	4.5	118	7	ADM05266	Adm05266 Human pro
152	6	4.5	80	5	ABG42731	Abg42731 Human pep	225	6	4.5	119	7	ADF59699	Adf59699 Human pol
153	6	4.5	81	3	AAI44083	Aai44083 Arabidops	226	6	4.5	120	7	ADE87014	Ade87014 Human pan
154	6	4.5	82	8	ADK47218	Adk47218 Streptoco	227	6	4.5	121	5	ABP09077	Abp09077 Human ORF
155	6	4.5	83	5	ABP00060	Abp00060 Human ORF	228	6	4.5	122	4	AAI5773	Aai5773 Human rep
156	6	4.5	83	7	ADF08024	Adf08024 Bacterial	229	6	4.5	122	4	ABB96304	Abb96304 Human tes
157	6	4.5	84	4	AAU86706	Aau86706 Novel hum	230	6	4.5	122	4	ABG60289	Abg60289 Human ova
158	6	4.5	84	4	ABM63828	Abm63828 Propionib	231	6	4.5	122	5	ABG61760	Abg61760 Novel ova
159	6	4.5	84	6	ABM60347	Abm60347 Propionib	232	6	4.5	124	3	AAI58722	Aai58722 Arabidops
160	6	4.5	84	7	ABU60040	Abu60040 Connectiv	233	6	4.5	124	4	AAU22406	Aau22406 Human car
161	6	4.5	85	5	ADH32539	Adh32539 Yeast smo	234	6	4.5	124	4	AAI42367	Aai42367 Human pol
162	6	4.5	86	4	ABB53005	Abb53005 Escherich	235	6	4.5	124	7	ADE46374	Ade46374 Human car
163	6	4.5	87	4	ABM61829	Abm61829 Propionib	236	6	4.5	124	8	ADJ07792	Adj07792 Human car
164	6	4.5	87	6	ABM58348	Abm58348 Propionib	237	6	4.5	125	5	ABP38617	Abp38617 Staphyloc
165	6	4.5	88	4	AAU14721	Aau14721 Novel bon	238	6	4.5	125	5	ABP51337	Abp51337 Human MDD
166	6	4.5	88	8	ADR40109	Adr40109 Human PKH	239	6	4.5	125	8	ADS05116	Ads05116 Staphyloc
167	6	4.5	90	4	AAO09955	Aao09955 Human pol	240	6	4.5	128	6	ABJ18793	Abj18793 Pseudomon
168	6	4.5	91	4	ABBI6571	Abbi6571 Human ner	241	6	4.5	129	3	AAU97865	Aau97865 Protein 1
169	6	4.5	92	2	AAI1535	Aai1535 M.ferment	242	6	4.5	133	3	AAI44082	Aai44082 Arabidops
170	6	4.5	93	5	ABG98438	Abg98438 Thermus t	243	6	4.5	133	5	ABP41276	Abp41276 Human ova
171	6	4.5	93	5	ABG73103	Abg73103 Human amy	244	6	4.5	133	5	ABP63803	Abp63803 Human ORF

245	6	4.5	133	8	ADR09540	Human pro	318	6	4.5	184	2	AAW90338	Human DPl
246	6	4.5	134	8	ADG22447	Cyanophag	319	6	4.5	184	3	AAI12151	Hydrophob
247	6	4.5	135	5	ABP34525	Human ORF	320	6	4.5	184	3	AAQ07200	Arabidops
248	6	4.5	136	2	AAW8980	Polypepti	321	6	4.5	184	3	AAQ48968	Arabidops
249	6	4.5	136	4	ABE51056	Human sec	322	6	4.5	184	3	AAQ07573	Arabidops
250	6	4.5	136	6	ABO45313	Novel hum	323	6	4.5	184	4	AAW38817	Human pol
251	6	4.5	136	7	ABO26793	Protein a	324	6	4.5	184	6	ABP70683	Rice acet
252	6	4.5	137	4	AAU53018	Propionib	325	6	4.5	184	7	ADC37437	Nuclear f
253	6	4.5	137	6	ABM69897	Phototrab	326	6	4.5	184	7	ADI63093	Human apo
254	6	4.5	137	6	ABM49537	Propionib	327	6	4.5	185	3	AAQ54086	Arabidops
255	6	4.5	138	3	AG21079	Arabidops	328	6	4.5	186	4	ABG02352	Novel hum
256	6	4.5	139	7	ABO70116	Pseudomon	329	6	4.5	186	7	ADC32800	Human nov
257	6	4.5	140	8	ADR99471	Chlamydia	330	6	4.5	188	7	ADC32822	Human nov
258	6	4.5	141	8	ADR99443	Chlamydia	331	6	4.5	189	3	AAQ49061	Arabidops
259	6	4.5	142	4	ABE11242	Human SLI	332	6	4.5	189	3	AAQ11287	Arabidops
260	6	4.5	142	4	AAO05847	Human pol	333	6	4.5	190	6	AAO16327	Human pol
261	6	4.5	142	7	ADP09329	Novel pro	334	6	4.5	191	4	ABE67425	Drosophil
262	6	4.5	142	7	ADP60617	Human con	335	6	4.5	191	4	ABG12181	Novel hum
263	6	4.5	142	8	ADR99387	Chlamydia	336	6	4.5	192	8	ABO586647	Human gen
264	6	4.5	144	3	AAQ55068	Arabidops	337	6	4.5	193	2	AAW23619	Prolactin
265	6	4.5	145	3	AAQ04272	Arabidops	338	6	4.5	197	3	AAQ23591	Arabidops
266	6	4.5	145	6	ADA34914	Acinetoba	339	6	4.5	197	6	ABU09847	Rat prola
267	6	4.5	147	3	AAQ44999	Zea mays	340	6	4.5	197	6	ADB08530	Alloiococ
268	6	4.5	147	6	ADB08528	Alloiococ	341	6	4.5	198	2	AAW22494	Rat prola
269	6	4.5	150	3	AAQ21078	Arabidops	342	6	4.5	198	6	ADA48256	Rice prot
270	6	4.5	151	2	AAQ37664	Protein w	343	6	4.5	198	6	ADA48574	Rice prot
271	6	4.5	152	2	AAQ35292	Chlamydia	344	6	4.5	199	4	AAW00877	Human bon
272	6	4.5	154	4	ABG12922	Novel hum	345	6	4.5	199	5	ABP41275	Human ova
273	6	4.5	154	7	ADP04497	Bacterial	346	6	4.5	200	4	AAW40603	Human pol
274	6	4.5	155	3	ADG15933	Arabidops	347	6	4.5	200	7	ADH85998	Enterococ
275	6	4.5	156	2	AAQ25008	Yeast YAP	348	6	4.5	202	2	AAQ39323	S. spinos
276	6	4.5	156	3	AAQ54087	Arabidops	349	6	4.5	202	4	AAW00896	Human bon
277	6	4.5	156	3	AAQ11288	Arabidops	350	6	4.5	202	6	ABU18571	Protein e
278	6	4.5	156	6	ABR53857	Protein s	351	6	4.5	202	6	ABU20918	Protein e
279	6	4.5	156	7	ADK64922	Disease t	352	6	4.5	202	6	ABU20869	Protein e
280	6	4.5	157	2	AAQ08307	Human CBC	353	6	4.5	205	4	ABW86168	A. thalia
281	6	4.5	157	3	AAQ04271	Arabidops	354	6	4.5	205	4	AAO06682	Human pol
282	6	4.5	157	4	AAU23312	Novel hum	355	6	4.5	206	7	ADC35090	Human bre
283	6	4.5	157	8	ADP24096	PRO polyp	356	6	4.5	207	4	ABG30286	Novel hum
284	6	4.5	158	8	ADK99291	Streptoco	357	6	4.5	207	4	ABG18189	Novel hum
285	6	4.5	159	4	ADG09853	Novel hum	358	6	4.5	207	5	ABP43634	FLJ20509
286	6	4.5	159	8	ADK16691	Nanoarcha	359	6	4.5	208	3	AAQ97386	Arabidops
287	6	4.5	160	2	AAQ37059	Protein i	360	6	4.5	208	4	AAW04153	Arabidops
288	6	4.5	160	6	ADA48584	Rice prot	361	6	4.5	208	5	AAE20526	Arabidops
289	6	4.5	160	6	ADA47984	Rice prot	362	6	4.5	208	5	AAE21532	Arabidops
290	6	4.5	161	4	ABG09854	Novel hum	363	6	4.5	208	5	ABW79064	Mature ar
291	6	4.5	164	3	AAQ21077	Arabidops	364	6	4.5	208	6	ABU11293	Arabidops
292	6	4.5	164	8	ADK99292	Streptoco	365	6	4.5	211	4	AAQ81246	Human AFP
293	6	4.5	165	7	ADC94956	E. faeciu	366	6	4.5	212	4	ADMI19920	Protein e
294	6	4.5	165	7	ADC94955	E. faeciu	367	6	4.5	213	4	AAW86945	Human 60S
295	6	4.5	166	6	ADA33772	Acinetoba	368	6	4.5	214	4	AAW86941	Human chr
296	6	4.5	168	4	AAQ02532	Human pol	369	6	4.5	214	4	AAW86942	Human chr
297	6	4.5	171	3	AAQ04270	Arabidops	370	6	4.5	214	6	AAO19616	Human nuc
298	6	4.5	173	3	AAQ15932	Arabidops	371	6	4.5	214	6	ABU24035	Protein e
299	6	4.5	177	4	AAU17268	Novel sig	372	6	4.5	214	7	ADB82785	Human pro
300	6	4.5	177	4	ABO30377	Human exp	373	6	4.5	214	8	ABM82464	Tumour-as
301	6	4.5	177	4	AAW96370	Human rep	374	6	4.5	214	8	ADP25310	PRO polyp
302	6	4.5	177	4	ABE10934	Human ova	375	6	4.5	215	6	ABP77878	N. gonorr
303	6	4.5	177	4	AAU87414	Novel cen	376	6	4.5	216	1	AAQ61024	Plasamid p
304	6	4.5	177	4	AAU87688	Novel cen	377	6	4.5	216	2	AAW11839	Sporamin
305	6	4.5	177	4	ADP93976	Human nov	378	6	4.5	217	4	AAE04102	Human gen
306	6	4.5	177	8	ADI54729	Novel hum	379	6	4.5	217	4	AAW41591	Human pol
307	6	4.5	177	8	ADI55003	Novel hum	380	6	4.5	217	5	ABG64382	Human alb
308	6	4.5	180	2	AAQ35323	Chlamydia	381	6	4.5	217	6	ADA41058	Human sec
309	6	4.5	180	4	AAE04177	Human gen	382	6	4.5	217	7	ADC74303	Human sec
310	6	4.5	180	6	ABU26771	Protein e	383	6	4.5	217	8	ADN17666	Albumin f
311	6	4.5	181	3	AAW41713	Human ORF	384	6	4.5	217	8	ADN17666	Bacterial
312	6	4.5	182	2	AAW48296	Human PGF	385	6	4.5	218	2	AAW99177	RasGAP ca
313	6	4.5	182	4	AAU29433	Human G p	386	6	4.5	218	2	AAW99162	RasGAP ca
314	6	4.5	182	5	ABG60721	Novel G p	387	6	4.5	218	4	AAE06613	Human pro
315	6	4.5	183	3	AAQ34111	Zea mays	388	6	4.5	218	4	ABW66330	Drosophil
316	6	4.5	183	5	ABP26401	Streptoco	389	6	4.5	218	5	ABR40479	Human sec
317	6	4.5	183	8	ADK99290	Streptoco	390	6	4.5	218	6	ABB82956	Human PRO

391	6	4.5	218	7	ADG75738	Adg75738	Human pro	464	6	4.5	240	3	AAG34109	Aag34109	Zea mays
392	6	4.5	219	1	AP61023	Ap61023	Plasmid p	465	6	4.5	240	3	AAG48966	Aag48966	Arabidops
393	6	4.5	219	2	AAR11802	Aar11802	Sporamin	466	6	4.5	240	3	AAG25606	Aag25606	Arabidops
394	6	4.5	219	4	AAE10856	Aae10856	Sweet pot	467	6	4.5	240	3	AAG07571	Aag07571	Arabidops
395	6	4.5	219	4	AAE04128	Aae04128	Human gen	468	6	4.5	240	5	ABB07959	Abb07959	Rat LR (r
396	6	4.5	219	4	AAE04127	Aae04127	Human gen	469	6	4.5	241	3	AAG49060	Aag49060	Arabidops
397	6	4.5	219	5	ASG64381	Asg64381	Human alb	470	6	4.5	241	4	ABG11558	Abg11558	Novel hum
398	6	4.5	219	5	ASG64380	Asg64380	Human alb	471	6	4.5	242	2	AAAY1194	Aay11194	S. pneumo
399	6	4.5	219	6	ADA41417	Ada41417	Human sec	472	6	4.5	242	3	AAAY1194	Aay11194	S. pneumo
400	6	4.5	219	6	ADA41418	Ada41418	Human sec	473	6	4.5	242	6	ABU02727	Abu02727	S. pneumo
401	6	4.5	219	7	ADC74551	Adc74551	Human sec	474	6	4.5	242	8	ADK47839	Adk47839	Streptoco
402	6	4.5	219	7	ADC74550	Adc74550	Human sec	475	6	4.5	243	5	ABP42317	Abp42317	Human ova
403	6	4.5	219	8	ADL77648	Adl77648	Albumin f	476	6	4.5	244	8	ADN17928	Adn17928	Bacterial
404	6	4.5	219	8	ADL77647	Adl77647	Albumin f	477	6	4.5	245	4	ABB65836	Abb65836	Drosophil
405	6	4.5	220	2	AAR60770	Aar60770	Maize QM	478	6	4.5	245	7	ADB65312	Adb65312	Human pro
406	6	4.5	220	2	AAAY05721	Aay05721	Gluconate	479	6	4.5	246	5	ABP38330	Abp38330	Staphyloc
407	6	4.5	220	3	AAG34110	Aag34110	Zea mays	480	6	4.5	246	8	ADS04851	Ads04851	Staphyloc
408	6	4.5	220	6	ABR52601	AbR52601	Protein s	481	6	4.5	247	6	ABM71082	Abm71082	Staphyloc
409	6	4.5	220	7	ADK63900	Adk63900	Disease t	482	6	4.5	248	3	AAG25605	Aag25605	Arabidops
410	6	4.5	220	8	ADS42682	Ads42682	Bacterial	483	6	4.5	248	4	ABB60027	Abb60027	Drosophil
411	6	4.5	221	3	AAG34633	Aag34633	Arabidops	484	6	4.5	249	3	AAB28001	Aab28001	Human sec
412	6	4.5	221	3	AAG07199	Aag07199	Arabidops	485	6	4.5	249	3	AAB28002	Aab28002	Human sec
413	6	4.5	221	3	AAG48967	Aag48967	Arabidops	486	6	4.5	252	4	AAG71966	Aag71966	Human olf
414	6	4.5	221	3	AAG07572	Aag07572	Arabidops	487	6	4.5	252	5	ABG60232	Abg60232	Human G p
415	6	4.5	221	6	ADA26318	Ada26318	Oncoprote	488	6	4.5	252	7	ADB70009	Adb70009	C. neofor
416	6	4.5	221	7	ABU62142	Abu62142	C-Jun N-t	489	6	4.5	254	7	ADC85615	Adc85615	Human GPC
417	6	4.5	221	7	ADJ64025	Adj64025	B-Jun N-t	490	6	4.5	257	8	ADR95157	Adr95157	Novel S.
418	6	4.5	222	3	AAAB16712	Aab16712	Bacteriop	491	6	4.5	258	6	ABU25091	Abu25091	Protein e
419	6	4.5	223	7	ADJ21645	Adj21645	Novel hum	492	6	4.5	260	2	AAV34541	Aay34541	Porphorym
420	6	4.5	223	7	ABO71431	AbO71431	Pseudomon	493	6	4.5	260	7	ADM47235	Adm47235	PK recept
421	6	4.5	223	8	ABO59832	AbO59832	Human gen	494	6	4.5	261	6	ABU21604	Abu21604	Protein e
422	6	4.5	224	3	AAG33417	Aag33417	Zea mays	495	6	4.5	262	4	AAU23380	Aau23380	Novel hum
423	6	4.5	224	7	ADE08523	Ade08523	Novel pro	496	6	4.5	262	4	AAU21782	Aau21782	Novel hum
424	6	4.5	225	1	AAAP82078	Aap82078	Recombina	497	6	4.5	262	7	ADC46423	Adc46423	Human neo
425	6	4.5	225	4	AAU18692	Aau18692	Renal and	498	6	4.5	264	2	AAR56499	Aar56499	TATA-bind
426	6	4.5	225	4	AAU20567	Aau20567	Human nov	499	6	4.5	264	2	AAW06089	Aaw06089	Human TAT
427	6	4.5	225	5	ABH78570	Abh78570	Human rib	500	6	4.5	264	2	AAW25016	Aaw25016	TATA-bind
428	6	4.5	225	5	ABH78570	Abh78570	Human rib	501	6	4.5	265	6	ABU11742	Abu11742	Human MDD
429	6	4.5	226	6	ABU97307	Abu97307	Human pol	502	6	4.5	266	2	AAV34407	Aay34407	Porphorym
430	6	4.5	226	2	AAAR14599	Aar14599	Rat prola	503	6	4.5	267	4	AAW80238	Aaw80238	Human pro
431	6	4.5	226	4	ABG12160	Abg12160	Novel hum	504	6	4.5	268	8	ADR66894	Adr66894	Human pro
432	6	4.5	226	6	ABU23549	Abu23549	Protein e	505	6	4.5	268	8	ADR65996	Adr65996	Human pro
433	6	4.5	229	4	AAG98977	Aag98977	E. coli g	506	6	4.5	270	3	AAG12989	Aag12989	Arabidops
434	6	4.5	229	6	ABR41691	AbR41691	Human DIT	507	6	4.5	270	3	AAG05237	Aag05237	Arabidops
435	6	4.5	229	8	ADK99196	Adk99196	Streptoco	508	6	4.5	270	3	AAG50049	Aag50049	Arabidops
436	6	4.5	229	8	ADK99197	Adk99197	Streptoco	509	6	4.5	271	3	AAV97392	Aay97392	Arabidops
437	6	4.5	230	8	ADK99195	Adk99195	Streptoco	510	6	4.5	271	3	AAG50048	Aag50048	Arabidops
438	6	4.5	230	8	ADK99194	Adk99194	Streptoco	511	6	4.5	271	3	AAG05236	Aag05236	Arabidops
439	6	4.5	232	6	ABU24519	Abu24519	Protein e	512	6	4.5	271	4	ABW04159	Abw04159	Arabidops
440	6	4.5	232	6	ABU23640	Abu23640	Protein e	513	6	4.5	271	5	AAE20532	Aae20532	Arabidops
441	6	4.5	233	3	AAV59412	Aay59412	Human CIP	514	6	4.5	271	5	AAE21538	Aae21538	Arabidops
442	6	4.5	233	4	ABG10183	Abg10183	Novel hum	515	6	4.5	271	5	AAE18646	Aae18646	Human G-p
443	6	4.5	233	7	ADJ68578	Adj68578	Human hea	516	6	4.5	271	5	ABB79070	Abb79070	Arabidops
444	6	4.5	233	7	ABM85809	Abm85809	Human pro	517	6	4.5	271	5	ABP65955	Abp65955	Bifidobac
445	6	4.5	233	8	ADO15479	Ado15479	Human Bcl	518	6	4.5	271	6	ABU11299	Abu11299	Arabidops
446	6	4.5	233	8	ADR87467	Adr87467	Rat B-cel	519	6	4.5	275	3	AAG34632	Aag34632	Arabidops
447	6	4.5	233	8	ADR87463	Adr87463	Human B-c	520	6	4.5	275	8	ADN46744	Adn46744	Thermococ
448	6	4.5	234	5	ABR40410	AbR40410	Human sec	521	6	4.5	276	5	ABP43635	Abp43635	FLJ20509
449	6	4.5	234	5	ADI28009	Adi28009	ECMCAL pr	522	6	4.5	277	4	AAW39805	Aaw39805	Human pol
450	6	4.5	234	6	ABR43632	AbR43632	Mouse CLA	523	6	4.5	279	6	ABU19100	Abu19100	Protein e
451	6	4.5	234	6	ADB11894	Abd11894	Alliococ	524	6	4.5	281	5	ABJ04730	Abj04730	GPCR 10 p
452	6	4.5	234	7	ADC95656	Adc95656	E. faeciu	525	6	4.5	284	3	AAG16499	Aag16499	Arabidops
453	6	4.5	234	7	ADI21249	Adi21249	Novel hum	526	6	4.5	284	3	AAG39487	Aag39487	Arabidops
454	6	4.5	234	8	ADK60179	Adk60179	Angiogene	527	6	4.5	284	4	AAE10804	Aae10804	A. thalia
455	6	4.5	234	8	ADK60480	Adk60480	Angiogene	528	6	4.5	284	6	ABU34729	Abu34729	Protein e
456	6	4.5	234	8	ADP73103	Adp73103	Angiogene	529	6	4.5	284	6	ABU35121	Abu35121	Protein e
457	6	4.5	235	3	AAG07198	Aag07198	Arabidops	530	6	4.5	284	6	ADA89376	Ada89376	A. thalia
458	6	4.5	235	4	ABG17696	Abg17696	Novel hum	531	6	4.5	285	2	AAW72751	Aaw72751	Streptoco
459	6	4.5	235	4	ABG18326	Abg18326	Novel hum	532	6	4.5	286	4	AAB86946	Aab86946	Human ak0
460	6	4.5	236	4	AAE04178	Aae04178	Human gen	533	6	4.5	286	4	AAB79376	Aab79376	Corynebac
461	6	4.5	237	2	AAW38641	Aaw38641	S. pneumo	534	6	4.5	287	5	AAO18609	Aao18609	Synechocy
462	6	4.5	238	3	AAG21622	Aag21622	Arabidops	535	6	4.5	287	8	ADS42462	Ads42462	Bacterial
463	6	4.5	238	5	ABB92058	Abb92058	Herbicida	536	6	4.5	289	2	AAV85811	Aay85811	S. pneumo

537	6	4.5	290	5	AB72326	Abb72326 Rat prote	610	322	7	ADB80350	Adb80350 Human MDD
538	6	4.5	290	7	ADM47237	Adm47237 NK recept	611	323	7	ADM03762	Adm03762 Human pro
539	6	4.5	294	3	AB32247	Ab32247 Tumour as	612	324	3	AA75254	Aa75254 Neisseria
540	6	4.5	294	4	AAU68912	Aau68912 Human TAG	613	324	3	AA75253	Aa75253 Neisseria
541	6	4.5	294	5	AAU78125	Aau78125 Human vom	614	324	3	AA75255	Aa75255 Neisseria
542	6	4.5	294	6	AAE37057	Aae37057 Human gen	615	324	6	ABP77231	Abp77231 N. gonorr
543	6	4.5	294	6	AAE37072	Aae37072 Human gen	616	325	7	ABO71675	Ab071675 Pseudomon
544	6	4.5	294	6	ABR40104	Ab40104 Human cel	617	326	4	AB60387	Ab60387 Human apo
545	6	4.5	294	7	ABE08376	Ab08376 Novel pro	618	326	5	ABB07263	Abb07263 Human apo
546	6	4.5	294	7	ADE13230	Ad013230 Human spl	619	326	5	ADC95799	Adc95799 E. faeciu
547	6	4.5	294	7	ADP05633	Adf05633 Bacterial	620	326	7	ADC73260	Adc73260 Human DED
548	6	4.5	294	7	ADH47211	Adm47211 Pheromone	621	327	2	AAR97845	Aar97845 Kaposi's
549	6	4.5	294	7	ADN95111	Adn95111 Human LEC	622	327	2	AAR93617	Aar93617 Kaposi's
550	6	4.5	294	8	ADH78439	Adh78439 Human tum	623	327	5	AA772093	Aa772093 Human ser
551	6	4.5	295	3	AG229139	Aag229139 Arabidops	624	327	5	ABG30790	Abg30790 Human ser
552	6	4.5	295	6	ABU48615	Abu48615 Protein e	625	327	5	AAE17921	Aae17921 Human gen
553	6	4.5	295	8	ADL04933	Adl04933 M. catarr	626	327	8	ADQ26095	Adq26095 Transmemb
554	6	4.5	296	8	ABO58743	Ab058743 Human gen	627	327	8	ADQ26096	Adq26096 Transmemb
555	6	4.5	297	3	AG229138	Aag229138 Arabidops	628	329	4	AAM89960	Aam89960 Human imm
556	6	4.5	297	8	ADS28869	Ad28869 Bacterial	629	332	6	ABU01726	Abu01726 S. pneumo
557	6	4.5	298	6	ABR82559	Ab82559 Human Chr	630	332	8	ADM92177	Adm92177 S. pneumon
558	6	4.5	298	7	ADD30540	Ad30540 Plant vie	631	335	6	ABU27128	Abu27128 Protein e
559	6	4.5	298	8	ADI44015	Adi44015 Plant tra	632	336	6	ABR42499	Ab42499 Coumernyc
560	6	4.5	300	2	AAVI6108	Aav16108 A formate	633	336	6	ABR42540	Ab42540 Clorobloc
561	6	4.5	300	7	ADH87377	Adh87377 Enterococ	634	336	7	ADJ94942	Adj94942 Novel NOV
562	6	4.5	303	4	AB60386	Ab60386 Human apo	635	336	7	ADJ94962	Adj94962 Novel NOV
563	6	4.5	304	3	AB15551	Ab15551 Apoptosis	636	336	8	ADO42203	Ado42203 Human NOV
564	6	4.5	304	3	AG333416	Aag333416 Zea may	637	336	8	ADO42207	Ado42207 Human NOV
565	6	4.5	305	8	ABM84152	Abm84152 Human dia	638	336	8	ADQ67568	Adq67568 Human hum
566	6	4.5	305	8	ADN19514	Adn19514 Bacterial	639	336	8	ADS10930	AdS10930 Human the
567	6	4.5	305	8	ADN17509	Adn17509 Bacterial	640	337	8	ADR10320	Adr10320 Human pro
568	6	4.5	307	2	AA84567	Aar84567 Trypanoso	641	338	3	AA616972	Aag16972 Arabidops
569	6	4.5	307	4	AG74832	Aag74832 Human col	642	338	6	ABP72962	Abp72962 Amino aci
570	6	4.5	307	4	AAU39710	Aau39710 Propionib	643	340	3	AA633415	Aag33415 Zea may
571	6	4.5	307	4	AG90155	Aag90155 C. Glutami	644	342	7	ADF76645	Adf76645 Novel hum
572	6	4.5	307	6	ABM36229	Abm36229 Propionib	645	342	8	ADJ66527	Adj66527 WD-repeat
573	6	4.5	308	2	AAW52194	Aaw52194 Human gly	646	342	8	ADS88398	AdS88398 Human pro
574	6	4.5	308	3	AG339486	Aag339486 Arabidops	647	342	8	ADN25409	Adn25409 Bacterial
575	6	4.5	308	4	AB92940	Ab92940 Human pro	648	344	7	ADD26726	Ad26726 Human adi
576	6	4.5	308	5	ABP27280	Abp27280 Streptoco	649	344	7	ADE13369	Ad013369 Human spl
577	6	4.5	308	5	ABF56625	Abf56625 Human ste	650	344	8	ADL31867	Adl31867 Human PRO
578	6	4.5	308	8	ADK99193	Adk99193 Streptoco	651	344	8	ADQ26097	Adq26097 Transmemb
579	6	4.5	308	8	ADS88208	AdS88208 Human pro	652	346	5	AAU74748	Aau74748 Human pro
580	6	4.5	309	3	AG16498	Aag16498 Arabidops	653	346	8	ADS24068	AdS24068 Bacterial
581	6	4.5	309	4	AG72262	Aag72262 Human olf	654	348	3	AA644528	Aag44528 Arabidops
582	6	4.5	309	4	AAU24707	Aau24707 Human olf	655	348	3	AA654097	Aag54097 Arabidops
583	6	4.5	309	5	ABF95840	Abf95840 Human GPC	656	348	3	AA654144	Aag54144 Arabidops
584	6	4.5	309	5	AAU85327	Aau85327 G-coupled	657	349	3	AA643785	Aag43785 Arabidops
585	6	4.5	309	6	ABU11156	Abu11156 Human G-p	658	349	7	ADM25918	Adm25918 Hyperther
586	6	4.5	309	7	ADC85743	Adc85743 Human GPC	659	350	3	AA643784	Aag43784 Arabidops
587	6	4.5	312	3	AG225604	Aag225604 Arabidops	660	351	3	AA654096	Aag54096 Arabidops
588	6	4.5	312	5	AAU95772	Aau95772 Human olf	661	351	3	AA644527	Aag44527 Arabidops
589	6	4.5	312	6	ABU11162	Abu11162 Human G-p	662	351	3	AA654143	Aag54143 Arabidops
590	6	4.5	312	6	AAO16329	Aao16329 Human pol	663	352	7	ADMA7229	Adm47229 NK recept
591	6	4.5	312	8	ADC85967	Adc85967 Human GPC	664	352	7	ADMA7227	Adm47227 NK recept
592	6	4.5	312	8	ADG83516	Adg83516 Human Olf	665	353	8	ADN18771	Adn18771 Bacterial
593	6	4.5	313	5	AAO17809	Aao17809 H. influen	666	354	7	ABM85235	Abm85235 Human pro
594	6	4.5	314	5	AAO16330	Aao16330 Human pol	667	354	8	ADN21071	Adn21071 Bacterial
595	6	4.5	316	5	ABP41228	Abp41228 Human ova	668	355	2	AAW72750	Aaw72750 Streptoco
596	6	4.5	317	5	ADE36453	Ad36453 Human PAN	669	355	5	ABP26355	Abp26355 Streptoco
597	6	4.5	317	5	ADM80187	Adm80187 Human NOV	670	355	6	ABU01818	Abu01818 S. pneumo
598	6	4.5	317	8	ADJ19375	Adj19375 Human PAN	671	355	7	ADH48628	Adh48628 3-dehydro
599	6	4.5	318	5	AAE24860	Aae24860 Human DED	672	355	7	ADH48630	Adh48630 Experimen
600	6	4.5	318	5	AAE38903	Aae38903 Human DED	673	355	8	ADK47027	Adk47027 Streptoco
601	6	4.5	318	6	ABU36529	Abu36529 Protein e	674	356	7	ADC96659	Adc96659 E. faeciu
602	6	4.5	318	6	ABR55201	Ab55201 Amino aci	675	360	3	AA593147	Aay59147 E. nidula
603	6	4.5	319	3	AB58420	Ab58420 Lung canc	676	360	3	ADJ70582	Adj70582 Human hea
604	6	4.5	320	5	ABG76848	Abg76848 Human G-p	677	360	8	ADS29093	AdS29093 Bacterial
605	6	4.5	321	3	AG34631	Aag34631 Arabidops	678	361	5	ABB91364	Abb91364 Herbicida
606	6	4.5	321	5	ABE90173	AbE90173 Human PAN	679	361	5	ABB06038	Abb06038 Human NS
607	6	4.5	321	8	ADJ19416	Adj19416 Human pol	680	361	8	ADR95298	Adr95298 Novel S.
608	6	4.5	322	6	ABM67907	Abm67907 Photorhab	681	364	2	AAW88979	Aaw88979 Polypepti
609	6	4.5	322	7	ABM74226	Abm74226 DNA clone	682	364	4	ABBS1055	Abbs1055 Human sec

683	6	4.5	364	6	ABO45312	Novel hum
684	6	4.5	364	7	ABO26792	Protein a
685	6	4.5	365	7	ADM47231	NK recept
686	6	4.5	366	4	AG73852	Humar. col
687	6	4.5	366	8	ADN24099	Bacterial
688	6	4.5	367	7	ADE08721	Novel pro
689	6	4.5	368	4	AAB88516	Haemcphil
690	6	4.5	368	5	ABO06039	Human. NS
691	6	4.5	368	5	AAU91447	Haemcphil
692	6	4.5	368	6	ABU49003	Protein e
693	6	4.5	368	6	ABU30152	Protein e
694	6	4.5	370	7	ADC26994	Sorangium
695	6	4.5	373	6	ABU29847	Protein e
696	6	4.5	373	7	ABO75799	Pseudomon
697	6	4.5	374	4	AAU34978	Enterococ
698	6	4.5	374	6	ABU29288	Protein e
699	6	4.5	374	8	ADS51929	TRMU SRQ
700	6	4.5	374	8	ADS51927	TRMU SRQ
701	6	4.5	375	4	ABB59643	Drocephil
702	6	4.5	376	5	ABP69074	Human pol
703	6	4.5	376	7	ADF06455	Bacterial
704	6	4.5	377	6	ABP57041	Leucnosc
705	6	4.5	382	7	ADH85944	Enterococ
706	6	4.5	383	7	ADF07147	Bacterial
707	6	4.5	385	4	ABB9162	Pucative
708	6	4.5	386	8	ADN25400	Bacterial
709	6	4.5	387	4	AAB61911	R. anatip
710	6	4.5	389	6	AAE32773	Mycobacte
711	6	4.5	389	6	ABU27679	Protein e
712	6	4.5	389	7	ADE47794	Human NOV
713	6	4.5	389	8	ADJ79064	Human NOV
714	6	4.5	390	3	ABJ42083	Human ORF
715	6	4.5	391	6	ABU49026	Protein e
716	6	4.5	392	6	ABU33486	Protein e
717	6	4.5	393	6	ABU45467	Protein e
718	6	4.5	394	5	ABP41994	Human ova
719	6	4.5	396	6	ABU49963	Protein e
720	6	4.5	396	7	ADM47225	NK recept
721	6	4.5	397	6	ABU31578	Protein e
722	6	4.5	397	6	ABU48064	Protein e
723	6	4.5	397	6	ABU15199	Protein e
724	6	4.5	397	6	ABU47088	Protein e
725	6	4.5	397	8	ABM84413	Human dia
726	6	4.5	398	4	ABBS9789	Drocephil
727	6	4.5	399	8	ABM84412	Human dia
728	6	4.5	400	4	ABG13840	Novel hum
729	6	4.5	400	7	ABO61409	Klebsiell
730	6	4.5	401	7	ABO78452	Pseudomon
731	6	4.5	402	6	ABU37636	Protein e
732	6	4.5	404	7	ADI21301	Novel hum
733	6	4.5	405	7	ABM74083	DNA clone
734	6	4.5	405	7	ADM25877	Hyperther
735	6	4.5	407	6	ABM67888	Phototrab
736	6	4.5	409	4	ABG21247	Novel hum
737	6	4.5	411	4	AAE12586	Pseudomon
738	6	4.5	412	4	ABG21571	Novel hum
739	6	4.5	419	6	ABU16307	Protein e
740	6	4.5	419	6	ABM72236	Staphyloc
741	6	4.5	419	8	ADH22284	ORF1 prot
742	6	4.5	422	2	AAW56275	Flavobact
743	6	4.5	424	6	ABU50519	Protein e
744	6	4.5	424	6	ABU32398	Protein e
745	6	4.5	425	2	AAW98019	Mouse cal
746	6	4.5	425	5	ABB99106	Mouse int
747	6	4.5	425	6	ABP56662	Chimpanze
748	6	4.5	426	4	AAI16773	Peptide #
749	6	4.5	426	4	ABB30593	Peptide #
750	6	4.5	426	4	AAW56567	Human bra
751	6	4.5	426	4	AAW04490	Peptide #
752	6	4.5	426	5	ABG38533	Human pep
753	6	4.5	428	6	ABU25307	Protein e
754	6	4.5	428	6	ABU29208	Protein e
755	6	4.5	428	7	ADM47233	NK recept

756	6	4.5	430	7	ADH87840	Enterococ
757	6	4.5	434	7	ADI21173	Novel hum
758	6	4.5	436	2	AAI35033	Chlamydia
759	6	4.5	438	7	AAO30835	Human cel
760	6	4.5	438	8	ABO84996	Murine hum
761	6	4.5	439	4	ABG17899	Novel hum
762	6	4.5	439	7	ABM85234	Mouse pro
763	6	4.5	439	8	ADN05434	Atipisori
764	6	4.5	441	5	ABP30345	Streptoco
765	6	4.5	442	4	ABW70328	Drosophil
766	6	4.5	442	7	ABO65176	Klebsiell
767	6	4.5	443	6	AAO23300	Chimpanze
768	6	4.5	443	6	AAO23297	Chimpanze
769	6	4.5	444	4	ABG30309	Novel hum
770	6	4.5	444	8	ADA44475	Bacterial
771	6	4.5	445	6	AAO23294	Chimpanze
772	6	4.5	448	3	AAO21060	Arbidiops
773	6	4.5	448	5	ABB93980	Herbicida
774	6	4.5	448	8	ADO70390	Unidentif
775	6	4.5	449	5	ABP28127	Streptoco
776	6	4.5	451	5	ABW47379	Listeria
777	6	4.5	451	6	AAU44258	Protein e
778	6	4.5	452	2	AAI41694	Human PRO
779	6	4.5	453	3	AAO44250	Human PRO
780	6	4.5	453	4	AAU29055	Human mem
781	6	4.5	453	4	AAE06935	Human ser
782	6	4.5	453	5	AAO18402	Human ser
783	6	4.5	453	5	ABJ05565	Breast ca
784	6	4.5	453	5	AAE23020	Human try
785	6	4.5	453	6	ABU58431	Human PRO
786	6	4.5	453	6	ABU87979	Novel hum
787	6	4.5	453	6	ABU84294	Human sec
788	6	4.5	453	6	ABR66168	Human sec
789	6	4.5	453	6	ABR65558	Human sec
790	6	4.5	453	6	ABU99498	Human sec
791	6	4.5	453	6	ABU82737	Human PRO
792	6	4.5	453	6	ABU98958	Novel hum
793	6	4.5	453	6	ABR58549	Human can
794	6	4.5	453	6	ABR68107	Human sec
795	6	4.5	453	6	ABU96160	Novel hum
796	6	4.5	453	6	ABU92591	Human sec
797	6	4.5	453	6	ABO08668	Human sec
798	6	4.5	453	6	ABO02720	Human sec
799	6	4.5	453	6	ABR74874	Human sec
800	6	4.5	453	6	ABR94636	Human sec
801	6	4.5	453	6	ABO25196	Novel hum
802	6	4.5	453	6	ABU89383	Human PRO
803	6	4.5	453	6	ABU85609	Human PRO
804	6	4.5	453	6	ABU98769	Novel hum
805	6	4.5	453	6	ABU97984	Novel hum
806	6	4.5	453	6	ABU91690	Novel hum
807	6	4.5	453	6	ABU72202	Novel hum
808	6	4.5	453	6	ABU86224	Human sec
809	6	4.5	453	6	ABU67437	Human sec
810	6	4.5	453	6	ABU80465	Human PRO
811	6	4.5	453	6	ABR99383	Human sec
812	6	4.5	453	6	ABR98773	Human sec
813	6	4.5	453	6	ABO16296	Human sec
814	6	4.5	453	6	ABR92196	Human sec
815	6	4.5	453	6	ABO18837	Human sec
816	6	4.5	453	6	ABR78258	Human sec
817	6	4.5	453	6	ABU56617	Lung canc
818	6	4.5	453	6	ABU84994	Novel hum
819	6	4.5	453	6	ABO00133	Novel hum
820	6	4.5	453	6	ABO11465	Human sec
821	6	4.5	453	6	ABO02110	Human sec
822	6	4.5	453	6	ABU88684	Novel hum
823	6	4.5	453	6	ABU83379	Human sec
824	6	4.5	453	6	ABO06180	Novel hum
825	6	4.5	453	6	ABO59216	Human sec
826	6	4.5	453	6	ABO09278	Human sec
827	6	4.5	453	6	ABO19142	Novel hum
828	6	4.5	453	6	ABO11160	Human sec

829	6	4.5	453	6	ABR66778	Human sec	902	6	4.5	453	6	ABO09888	Human sec
830	6	4.5	453	6	ABO15991	Human sec	903	6	4.5	453	6	ABO08973	Human sec
831	6	4.5	453	6	ABO13697	Human sec	904	6	4.5	453	6	ABU10541	Human sec
832	6	4.5	453	6	ABU84882	Human sec	905	6	4.5	453	6	ABU95550	Human PRO
833	6	4.5	453	6	ABU65600	Human sec	906	6	4.5	453	6	ABU96759	Novel hum
834	6	4.5	453	6	ABO07448	Human PRO	907	6	4.5	453	6	ABR70604	Human sec
835	6	4.5	453	6	ABO03635	Human sec	908	6	4.5	453	6	ABO04955	Novel hum
836	6	4.5	453	6	ABR67083	Human sec	909	6	4.5	453	6	ABO08363	Human sec
837	6	4.5	453	6	ABU15686	Human sec	910	6	4.5	453	6	ABO05570	Human sec
838	6	4.5	453	6	ABU55967	Human sec	911	6	4.5	453	6	ABR73959	Human sec
839	6	4.5	453	6	ABU61080	Human PRO	912	6	4.5	453	6	ABR95551	Human sec
840	6	4.5	453	6	ABU65295	Human PRO	913	6	4.5	453	6	ABR80848	Human sec
841	6	4.5	453	6	ABU95240	Novel hum	914	6	4.5	453	6	ABR81153	Human sec
842	6	4.5	453	6	ABU71143	Human PRO	915	6	4.5	453	6	ABM00849	Human sec
843	6	4.5	453	6	ABO07753	Human PRO	916	6	4.5	453	6	ABR88451	Human sec
844	6	4.5	453	6	ABR69994	Human sec	917	6	4.5	453	6	ABM77272	Human sec
845	6	4.5	453	6	ABR69327	Human sec	918	6	4.5	453	6	ABO28756	Human sec
846	6	4.5	453	6	ABO01468	Human PRO	919	6	4.5	453	6	ABO31501	Human sec
847	6	4.5	453	6	ABU81270	Human PRO	920	6	4.5	453	6	ABM07918	Human sec
848	6	4.5	453	6	ABR60067	Human sec	921	6	4.5	453	6	ABO40398	Human sec
849	6	4.5	453	6	ABR67802	Human sec	922	6	4.5	453	6	ABO35823	Human PRO
850	6	4.5	453	6	ABR65190	Human sec	923	6	4.5	453	6	ABO43962	Human PRO
851	6	4.5	453	6	ABR68412	Human sec	924	6	4.5	453	6	ADA77816	Human sec
852	6	4.5	453	6	ABR71824	Human sec	925	6	4.5	453	6	ABM24757	Human sec
853	6	4.5	453	6	ABU85304	Human PRO	926	6	4.5	453	6	ABO03025	Human sec
854	6	4.5	453	6	ABU88994	Human sec	927	6	4.5	453	6	ABR90281	Human sec
855	6	4.5	453	6	ABU83074	Human sec	928	6	4.5	453	6	ABM17195	Human sec
856	6	4.5	453	6	ABU94930	Novel hum	929	6	4.5	453	6	ABU62146	Tumour-ab
857	6	4.5	453	6	ABU90478	Novel hum	930	6	4.5	453	6	ABR94941	Human sec
858	6	4.5	453	6	ABU83989	Human sec	931	6	4.5	453	6	ABR95246	Human sec
859	6	4.5	453	6	ABU93640	Novel hum	932	6	4.5	453	6	ABO21148	Human sec
860	6	4.5	453	6	ABR64885	Human sec	933	6	4.5	453	6	ABR97748	Human sec
861	6	4.5	453	6	ABR68717	Human sec	934	6	4.5	453	6	ABR87536	Human sec
862	6	4.5	453	6	ABO06533	Human sec	935	6	4.5	453	6	ABM77577	Human sec
863	6	4.5	453	6	ABR99078	Human sec	936	6	4.5	453	6	ABM27807	Human sec
864	6	4.5	453	6	ABU56962	Human PRO	937	6	4.5	453	6	ABM06088	Human sec
865	6	4.5	453	6	ABU85914	Novel hum	938	6	4.5	453	6	ABM03594	Human sec
866	6	4.5	453	6	ABU82201	Novel hum	939	6	4.5	453	6	ABM35045	Human sec
867	6	4.5	453	6	ABU87212	Human PRO	940	6	4.5	453	6	ABM26282	Human sec
868	6	4.5	453	6	ABU83684	Human sec	941	6	4.5	453	6	ABO48064	Human sec
869	6	4.5	453	6	ABO08058	Human PRO	942	6	4.5	453	6	ABR92806	Human sec
870	6	4.5	453	6	ABU81769	Novel hum	943	6	4.5	453	6	ABO24567	Human sec
871	6	4.5	453	6	ABU65933	Novel hum	944	6	4.5	453	6	ABM11578	Human sec
872	6	4.5	453	6	ABR59762	Human sec	945	6	4.5	453	6	ABM02679	Human sec
873	6	4.5	453	6	ABU93950	Novel hum	946	6	4.5	453	6	ABM15975	Human sec
874	6	4.5	453	6	ABU80349	Human sec	947	6	4.5	453	6	ABO27536	Human sec
875	6	4.5	453	6	ABU99803	Novel hum	948	6	4.5	453	6	ABM29027	Human sec
876	6	4.5	453	6	ABR66473	Human sec	949	6	4.5	453	6	ABM07003	Human sec
877	6	4.5	453	6	ABR90891	Human sec	950	6	4.5	453	6	ABM21097	Human sec
878	6	4.5	453	6	ABU94318	Human PRO	951	6	4.5	453	6	ABM09443	Human sec
879	6	4.5	453	6	ABU79200	Human PRO	952	6	4.5	453	6	ABO41313	Human sec
880	6	4.5	453	6	ABU86529	Human sec	953	6	4.5	453	6	ABO36128	Human PRO
881	6	4.5	453	6	ABU86834	Novel hum	954	6	4.5	453	6	ABO43657	Human PRO
882	6	4.5	453	6	ABU94623	Human PRO	955	6	4.5	453	6	ABM76357	Human sec
883	6	4.5	453	6	ABO04550	Human PRO	956	6	4.5	453	6	ABM76053	Human sec
884	6	4.5	453	6	ABR70299	Human sec	957	6	4.5	453	6	ABM25672	Human sec
885	6	4.5	453	6	ABU98464	Human PRO	958	6	4.5	453	6	ABM25977	Human sec
886	6	4.5	453	6	ABR65863	Human sec	959	6	4.5	453	6	ABO03330	Human sec
887	6	4.5	453	6	ABR64580	Human sec	960	6	4.5	453	6	ABO02415	Human sec
888	6	4.5	453	6	ABU79505	Human PRO	961	6	4.5	453	6	ABR90586	Human sec
889	6	4.5	453	6	ABU92896	Human sec	962	6	4.5	453	6	ABR73654	Human sec
890	6	4.5	453	6	ABU95855	Human PRO	963	6	4.5	453	6	ABO16906	Human sec
891	6	4.5	453	6	ABU91075	Novel hum	964	6	4.5	453	6	ABR94331	Human sec
892	6	4.5	453	6	ABU90168	Novel hum	965	6	4.5	453	6	ABR75838	Human sec
893	6	4.5	453	6	ABO09583	Human sec	966	6	4.5	453	6	ABR71214	Human sec
894	6	4.5	453	6	ABO10855	Human sec	967	6	4.5	453	6	ABR93111	Human sec
895	6	4.5	453	6	ABR70909	Human sec	968	6	4.5	453	6	ABR93416	Human sec
896	6	4.5	453	6	ABU87517	Human PRO	969	6	4.5	453	6	ABR87841	Human sec
897	6	4.5	453	6	ABU91385	Human PRO	970	6	4.5	453	6	ABO27841	Human sec
898	6	4.5	453	6	ABU84599	Human sec	971	6	4.5	453	6	ABO29976	Human sec
899	6	4.5	453	6	ABR69689	Human sec	972	6	4.5	453	6	ABO33185	Human PRO
900	6	4.5	453	6	ABU80066	Human PRO	973	6	4.5	453	6	ABM04873	Human sec
901	6	4.5	453	6	ABU93335	Human PRO	974	6	4.5	453	6	ABM08833	Human sec

PT New TRAF-protein binding domain polypeptide, useful e.g. for treatment
PT and diagnosis of cancer or autoimmune diseases, also related nucleic acid
PT and modulators.

PS Claim 4; Page 131-132; 156pp; English.

XX The present sequence is human speckle-type POZ protein (SPOP) TRAF
CC (tumour necrosis factor, TNF receptor-associated factor)-protein binding
CC domain (TPBD) protein. TPBDs and/or anti-TPBD antibodies (Ab) are used to
CC identify agents for treatment of autoimmune diseases, inflammation,
CC allergy, allograft rejection, sepsis, cancers such as gliomas, leukaemias
CC carcinomas, adenocarcinomas, sarcomas, melanomas, hamartomas, leukaemias
CC and lymphomas, benign proliferative diseases, benign prostatic
CC hypertrophy, keratinocyte hyperplasia, neoplasia, keloid, inflammatory
CC following balloon angioplasty (restenosis), bone marrow aplasia or
CC generally any condition that involves abnormal apoptosis, cellular
CC proliferation, differentiation or stress responses or immunoglobulin
CC class switching in B cells. Agents (Ab or oligonucleotides) that bind
CC specifically to TPBD or its nucleic acid are useful for diagnosis of the
CC specified diseases, particularly for diagnosis or prognosis of cancer or
CC for monitoring therapy

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 132; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.5e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCREMGVIVKSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 60
Db 33 SYMTINNFSFCREMGVIVKSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 92
Qy 61 CPKSEVRKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
Db 93 CPKSEVRKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 152
Qy 121 DKLTFLFCEVSVV 132
Db 153 DKLTFLFCEVSVV 164

RESULT 3
AAB90799
ID AAB90799 standard; protein; 374 AA.

XX AAB90799;
XX 15-JUN-2001 (first entry)
XX Human shear stress-response protein SEQ ID NO: 98.

XX Human; shear stress-response protein; vascular disease; arteriosclerosis.
XX Homo sapiens.

XX WO200125427-A1.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-JP006840.

XX 01-OCT-1999; 93JP-00280976.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX (NOJI/) NOJIMA H.

XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;

XX Kuga T, Sekine S, Nakamura Y, Sugano S;

XX WPI; 2001-266308/27.

XX N-PSDB; AAB02922.

PT DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis.

PS Claim 60; Page 503-505; 678pp; Japanese.

XX The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension

XX SQ Sequence 374 AA;

Query Match 100.0%; Score 132; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCREMGVIVKSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 60
Db 33 SYMTINNFSFCREMGVIVKSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 92
Qy 61 CPKSEVRKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
Db 93 CPKSEVRKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 152
Qy 121 DKLTFLFCEVSVV 132
Db 153 DKLTFLFCEVSVV 164

RESULT 4

AAB03659

ID AAB03659 standard; protein; 374 AA.

XX AAB03659;

XX 29-AUG-2001 (first entry)

XX Human SPOP TRAF-protein binding domain (TPBD) protein #1.

XX Human; speckle-type POZ protein; SPOP; therapy; tumour necrosis factor;
XX TNF receptor-associated factor; adenocarcinoma; autoimmune disease;
XX TRAF-protein binding domain; TPBD; allergy; cancer; allograft rejection;
XX sepsis; glioma; carcinoma; sarcoma; melanoma; hamartoma; leukaemia;
XX lymphoma; neoplasia; benign proliferative disease; restenosis; fibrosis;
XX keratinocyte hyperplasia; benign prostatic hypertrophy; keloid;
XX inflammatory hyperplasia; balloon angioplasty; bone marrow aplasia;
XX stress response; cellular proliferation; immunoglobulin class switching;
XX Ig; apoptosis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..180

XX /note= "TRAF-protein binding domain fragment"

XX WO200132696-A2.

XX 10-MAY-2001.

XX 03-NOV-2000; 2000WO-US030533.

XX 05-NOV-1999; 99US-00434784.

XX (BURN-) BURNHAM INST.

XX Zapata JM, Reed JC;

XX WPI; 2001-381115/40.

XX N-PSDB; AAD08067.

XX New TRAF-protein binding domain polypeptide, useful e.g. for treatment

PT and diagnosis of cancer or autoimmune diseases, also related nucleic acid
 PT and modulators.

PS Claim 57; Page 116-117; 156pp; English.

XX The present sequence is human speckle-type POZ protein (SPOP) TRAF
 CC (tumour necrosis factor, TNF receptor-associated factor)-protein binding
 CC domain (TPBD). TPBDs and/or anti-TPBD antibodies (Ab) are used to
 CC identify agents for treatment of autoimmune diseases, inflammation,
 CC allergy, allograft rejection, sepsis, cancers such as gliomas,
 CC carcinomas, adenocarcinomas, sarcomas, melanomas, hamartomas, leukaemias
 CC and lymphomas, benign proliferative diseases, benign prostatic
 CC hypertrophy, keratinocyte hyperplasia, neoplasia, keloid, inflammatory
 CC hyperplasia, fibrosis, smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis), bone marrow aplasia or
 CC generally any condition that involves abnormal apoptosis, cellular
 CC proliferation, differentiation or stress responses or immunoglobulin
 CC class switching in B cells. Agents (Ab or oligonucleotides) that bind
 CC specifically to TPBD or its nucleic acid are useful for diagnosis of the
 CC specified diseases, particularly for diagnosis or prognosis of cancer or
 CC for monitoring therapy

XX Sequence 374 AA;

Query Match 100.0%; Score 132; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.9e-137;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLLVLS 60
 DB 33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLLVLS 92
 QY 61 CPKSEVRAKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
 DB 93 CPKSEVRAKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 152
 QY 121 DKLTLCFCEVSVV 132
 DB 153 DKLTLCFCEVSVV 164

RESULT 5

ADB85287
 ID ADB85287 standard; protein; 374 AA.
 XX ADB85287;
 AC ADB85287;
 DT 04-DEC-2003 (first entry)
 XX Human prosaposin SEQ ID NO:168.
 DE
 XX rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;
 KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;
 KW protease; enzyme; analgesic; gene therapy; pain; diabetes.
 OS Rattus norvegicus.
 XX
 XX EP1284297-A2.
 FN
 XX
 XX 19-FEB-2003.
 PD
 XX
 XX 26-JUL-2002; 2002EP-00255228.
 PF
 XX
 XX 27-JUL-2001; 2001GB-00018354.
 PR
 XX 07-FEB-2002; 2002GB-00002880.
 PR
 XX
 XX (WARN) WARNER LAMBERT CO.
 PA
 XX
 XX Brooksbank RA, Dixon AK, Lee K, Finnock RD;
 FI
 XX WPI; 2003-364994/35.
 DR
 XX N-PSDB; ADB85288.
 DR
 XX

PT Use of gene sequence that is down-regulated in response to streptozocin-
 PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in
 PT screening of compounds for treating or diagnosing pain.

XX Disclosure; Page 243-244; 256pp; English.

PS The invention relates to a novel isolated gene sequence that is down-
 CC regulated in the spinal cord in response to streptozocin-induced
 CC diabetes, or comprising, hybridising or having at least 80% sequence
 CC identity to a sequence whose expression products are kinases,
 CC phosphatases, ion channel proteins, receptors, transporters, G-protein
 CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,
 CC given in the specification. A gene of the invention has analgesic
 CC activity, and may have a use in gene therapy. The gene sequences, vector,
 CC host cell, animal, polypeptide and antibody are useful for screening of
 CC compounds for diagnosing or treating pain. The kits are useful for
 CC simultaneous, separate or sequential detecting and/or quantifying down-
 CC regulation of a gene sequence in the spinal cord of a mammal in response
 CC to streptozocin-induced diabetes. The compound or pharmaceutical
 CC composition is useful as a medicament for treating or diagnosing pain.
 CC The present sequence represents a protein encoded by a gene of the
 CC invention.

XX Sequence 374 AA;

Query Match 100.0%; Score 132; DB 7; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.9e-137;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLLVLS 60
 DB 33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLLVLS 92
 QY 61 CPKSEVRAKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
 DB 93 CPKSEVRAKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 152
 QY 121 DKLTLCFCEVSVV 132
 DB 153 DKLTLCFCEVSVV 164

RESULT 6

ADI62718
 ID ADI62718 standard; protein; 374 AA.
 XX ADI62718;
 AC ADI62718;
 DT 22-APR-2004 (first entry)
 XX Human apoptosis-associated protein SEQ ID 161.
 DE
 XX apoptosis; cell death; cystostatic; neuroprotective; immunosuppressive;
 KW antirheumatic; antiarthritic; dermatological; antiinflammatory;
 KW hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian;
 KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;
 KW autoimmune disease; degenerative disease; viral infection; leukaemia;
 KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;
 KW lupus; hepatitis; influenza viruses; Alzheimer's disease;
 KW Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;
 KW alcoholic liver disease; human.
 XX
 XX Homo sapiens.
 OS
 XX WO2003058021-A2.
 FN
 XX
 XX 17-JUL-2003.
 PD
 XX
 XX 13-JAN-2003; 2003WO-EP000270.
 PF
 XX
 XX 11-JAN-2002; 2002DE-01000856.
 PR
 XX
 XX (XANT-) XANTOS BIOMEDICINE AG.
 PA

XX Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;
XX WPI; 2003-542134/51.
XX N-PSDB; ADI62616.
XX
XX New nucleic acids involved in apoptosis, useful for diagnosis and
XX treatment of e.g. tumors and degenerative disease, also related proteins,
XX antibodies and modulators.
XX
XX Claim 1a; SEQ ID NO 161; 517pp; German.
XX
XX This invention describes novel nucleic acid molecules that are associated
XX with apoptosis and encode a polypeptide and are derived from a normalised
XX gene library (embryonic or liver) or clone collections, and the extent of
XX apoptosis measured by cell death detection assay or the CPRG assay
XX (measuring loss of membrane integrity). The products of the invention
XX have cytostatic, neuroprotective, immunosuppressive, antirheumatic,
XX antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,
XX neurotropic, anticonvulsant, antiparkinsonian, vasotropic,
XX cerebroprotective and antialcoholic activity and can be used for gene
XX therapy. The polynucleotides also related vectors, hosts (or their
XX extracts), encoded polypeptide (or their receptors) and/or agents that
XX inhibit their activity (including antisense sequences) are used for
XX treatment or prevention of tumours, autoimmune or degenerative diseases
XX and viral infections, specifically leukaemia, carcinoma, sarcoma,
XX multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection
XX with hepatitis or influenza viruses, Alzheimer's, Huntington's or
XX Parkinson's diseases, reperfusion injury, stroke and alcoholic liver
XX disease. Detection of the polynucleotides and derived polypeptides can
XX also be used for diagnosis of these diseases. This sequence represents an
XX apoptosis-associated protein described in the invention.
XX
XX Sequence 374 AA;
XX
XX Query Match 100.0%; Score 132; DB 7; Length 374;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-137;
XX Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLSLYLLVLS 60
XX Db 33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLSLYLLVLS 92
XX
XX Qy 61 CPKSEVRAPKFSILNAKGETKAMESORAYRFVQGDWGFKFIIRDFLLDEANGLLPD 120
XX Db 93 CPKSEVRAPKFSILNAKGETKAMESORAYRFVQGDWGFKFIIRDFLLDEANGLLPD 152
XX
XX Qy 121 DKLTFLFCEVSVV 132
XX Db 153 DKLTFLFCEVSVV 164
XX
XX RESULT 7
XX ADQ89936
XX ID ADQ89936 standard; protein; 374 AA.
XX AC ADQ89936;
XX
XX 21-OCT-2004 (first entry)
XX
XX Antagonist of cell cycle progression polypeptide #183.
XX
XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
XX cell cycle progression.
XX
XX Homo sapiens.
XX
XX WO2004063362-A2.
XX
XX 29-JUL-2004.
XX
XX 31-DEC-2003; 2003WO-GB005635.
XX
XX 29-JUL-2004.
XX
XX 31-DEC-2003; 2003WO-GB005635.

PR 10-JAN-2003; 2003US-0439123P.
PR 06-MAY-2003; 2003US-0468402P.
XX
XX (CYCL-) CYCLACEL LTD.
XX
XX Glover D, Bell G, Frenz L, Midgley C;
XX
XX WPI; 2004-544089/52.
XX N-PSDB; ADQ89935.
XX
XX New cell cycle progression genes and proteins for modulating cell cycle
XX progression in cells, for preventing, treating or diagnosing cell
XX proliferative diseases (e.g. cancer) or for identifying modulators of
XX mitosis or meiosis.
XX
XX Claim 2; SEQ ID NO 366; 461pp; English.
XX
XX The present invention relates to a polynucleotide for preventing,
XX treating or diagnosing a disease in an individual. The composition or the
XX polypeptide, polynucleotide or RNA precursor, or antibody is useful for
XX diagnosing, preventing or treating diseases (e.g. cell proliferative
XX diseases such as cancer) in an individual. These may also be used for
XX identifying substances capable of binding to or modulating the function
XX of the polypeptide, capable of affecting the function of the
XX corresponding gene, or capable of inhibiting the cell division cycle or
XX cell cycle progression, preferably mitosis and/or meiosis. The present
XX sequence represents an antagonist of cell cycle progression protein
XX sequence.
XX
XX Sequence 374 AA;
XX
XX Query Match 100.0%; Score 132; DB 8; Length 374;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-137;
XX Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLSLYLLVLS 60
XX Db 33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLSLYLLVLS 92
XX
XX Qy 61 CPKSEVRAPKFSILNAKGETKAMESORAYRFVQGDWGFKFIIRDFLLDEANGLLPD 120
XX Db 93 CPKSEVRAPKFSILNAKGETKAMESORAYRFVQGDWGFKFIIRDFLLDEANGLLPD 152
XX
XX Qy 121 DKLTFLFCEVSVV 132
XX Db 153 DKLTFLFCEVSVV 164
XX
XX RESULT 8
XX ADQ89928
XX ID ADQ89928 standard; protein; 374 AA.
XX AC ADQ89928;
XX
XX 21-OCT-2004 (first entry)
XX
XX Antagonist of cell cycle progression polypeptide #179.
XX
XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
XX cell cycle progression.
XX
XX Homo sapiens.
XX
XX WO2004063362-A2.
XX
XX 29-JUL-2004.
XX
XX 31-DEC-2003; 2003WO-GB005635.
XX
XX 10-JAN-2003; 2003US-0439123P.
XX 06-MAY-2003; 2003US-0468402P.
XX
XX (CYCL-) CYCLACEL LTD.
XX

XX
PI Glover D, Bell G, Frenz L, Midgley C;
XX WPI; 2004-544089/52.
DR N-PSDB; ADQ89927.
XX
XX New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
XX Claim 2; SEQ ID NO 358; 461pp; English.
PS
XX The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
CC sequence.
XX
SQ Sequence 374 AA;
Query Match 100.0%; Score 132; DB 8; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCREEMGEVSKSTFSSGANDKLKWLVRNPKGLDESKDYLSYLLVLS 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
33 SYMTINNFSFCREEMGEVSKSTFSSGANDKLKWLVRNPKGLDESKDYLSYLLVLS 92
Qy 61 CPKSEVRKPKFSILNAKGETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
93 CPKSEVRKPKFSILNAKGETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 152
Qy 121 DKLTLCFCEVSVV 132
Db ||||||||||||||||
153 DKLTLCFCEVSVV 164
RESULT 9
AAB58286
ID AAB58286 standard; protein; 395 AA.
AC AAB58286;
XX
XX 14-MAR-2001 (first entry)
XX
XX Lung cancer associated polypeptide sequence SEQ ID 624.
DE
XX Human; lung cancer associated protein; neuroprotective; cytoskeletal;
KW cardiac; immunomodulatory; muscular active; vulnerable;
KW gastrointestinal; nephrotropic; anti-infective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease.
XX
XX Homo sapiens.
XX
XX WO200055180-A2.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005918.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX

PI Ruben SM;
XX
DR WPI; 2000-587514/55.
DR N-PSDB; AAF18162.
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer.
XX
XX Claim 11; Page 1117-1119; 1425pp; English.
PS
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC immunomodulators may have neuroprotective, cytoskeletal, cardiac, and
CC general; nephrotropic; anti-infective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the protein
CC or polynucleotide sequences. The lung cancer associated polynucleotide
CC sequences may be used for detection of lung cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The proteins may be used to treat disorders such as
CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
CC cardiovascular, renal, and proliferative disorders. The proteins may also
CC be used in the treatment of wounds and infectious diseases.
CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
CC used in the course of the invention for the identification and
CC characterisation of the polynucleotide and protein sequences
XX
SQ Sequence 385 AA;
Query Match 100.0%; Score 132; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.1e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCREEMGEVSKSTFSSGANDKLKWLVRNPKGLDESKDYLSYLLVLS 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
44 SYMTINNFSFCREEMGEVSKSTFSSGANDKLKWLVRNPKGLDESKDYLSYLLVLS 103
Qy 61 CPKSEVRKPKFSILNAKGETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
104 CPKSEVRKPKFSILNAKGETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 163
Qy 121 DKLTLCFCEVSVV 132
Db ||||||||||||||||
164 DKLTLCFCEVSVV 175
RESULT 10
ABG23713
ID ABG23713 standard; protein; 398 AA.
XX
XX ABG23713;
XX
XX 18-FEB-2002 (first entry)
DT
XX Novel human diagnostic protein #23704.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US008631.
PF
XX 31-MAR-2000; 2000US-00540217.
PR
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA

CC supplements. These are useful in gene therapy, particularly for treating
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC inflammation. The nucleic acids and polypeptides are also useful in
CC diagnostic and research methods. The sequences given in records ABP43544-
CC ABP43989 represent polypeptides encoded by polynucleotides of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 392 AA;

Query Match 40.2%; Score 53; DB 5; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.3e-49;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQKDWGFKFIRDRDFLLDEANGLLPDDKLTLCFESVW 132
|||||
Db 112 EETKAMESQRAYRFVQKDWGFKFIRDRDFLLDEANGLLPDDKLTLCFESVW 164

RESULT 15

ABU96687
ID ABU96687 standard; protein; 392 AA.

XX AC ABU96687;

XX DT 25-JUL-2003 (first entry)

XX DE Human nucleic acid-associated protein (NAAP) #16.

XX KW Human; nucleic acid-associated protein; cytostatic; antiarteriosclerotic;
XX KW anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV;
XX KW anti-allergic; anti-inflammatory; thymimetic; gene therapy;
XX KW cell proliferative disorder; cancer; atherosclerosis;
XX KW neurological disorder; epilepsy; Huntington's disease; stroke;
XX KW immune disorder; inflammatory disorder; AIDS; allergy;
XX KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
XX KW protein-protein interaction; drug-target interaction;
XX KW gene expression profile.

XX OS Homo sapiens.

XX PN WO2003023003-A2.

XX XX 20-MAR-2003.

XX XX 05-SEP-2002; 2002WO-US028540.

XX XX 07-SEP-2001; 2001US-0317792P.

XX XX 07-SEP-2001; 2001US-0317912P.

XX XX 14-SEP-2001; 2001US-0322270P.

XX XX 21-SEP-2001; 2001US-0324040P.

XX XX 28-SEP-2001; 2001US-0326732P.

XX XX 19-OCT-2001; 2001US-0346716P.

XX XX 25-JAN-2002; 2002US-0351749P.

XX XX 22-FEB-2002; 2002US-0359498P.

XX XX (INCY-) INCYTE GENOMICS INC.

XX PI Tang YT, Jackson JL, Griffin JA, Elliott VS, Forsythe IJ;

XX PI Becha SD, Richardson TW, Lee EA, Sprague WW, Emerling BM;

XX PI Thangavelu K, Warren EA, Tran UK, Yue H, Xu Y, Yue H, Li JX;

XX PI Hafalia AJA, Sanjanwala B, Marquis JP, Gorvad AE, Lee SY, Ison CH;

XX PI Baughn MR, Chawla NK, Nguyen DB, Swarnakar A, Zebardjian Y, Shah P;

XX PI Thornton M, Yao MG, Khan FA, Gandhi AR, Yang J, Kable AE;

XX PI Burford N, Ramkumar J;

PT aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
PT infections.

XX PS Claim 1; Page 253; 345pp; English.

XX CC The invention describes a novel human isolated nucleic acid-associated
XX polypeptide (NAAP). The polypeptides and polynucleotides are useful in
XX diagnosing, treating and preventing diseases or conditions associated
XX with the decreased expression or overexpression of NAAP, such as cell
XX proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
XX epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
XX allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome),
XX disorders, or infections. These are also useful in assessing the effects
XX of exogenous compounds on the expression of nucleic acid and amino acid
XX sequences of NAAP. The NAAP or its fragments are useful in screening
XX compounds for effectiveness as agonist or antagonist of the polypeptides,
XX or in altering the expression of the target polynucleotide and compounds
XX that specifically bind to or modulate the activity of the polypeptide.

XX CC The microarray is useful in monitoring or measuring protein-protein
XX interactions, drug-target interactions, and gene expression profiles.
XX CC This is the amino acid sequence of a novel human nucleic acid-associated
XX protein (NAAP)

XX SQ Sequence 392 AA;

Query Match 40.2%; Score 53; DB 6; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.3e-49;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQKDWGFKFIRDRDFLLDEANGLLPDDKLTLCFESVW 132
|||||
Db 112 EETKAMESQRAYRFVQKDWGFKFIRDRDFLLDEANGLLPDDKLTLCFESVW 164

Search completed: July 20, 2005, 20:47:39
Job time : 128.457 secs

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:52:32 ; Search time 83.9143 Seconds

(without alignments)
610.633 Million cell updates/sec

Title: US-09-706-325-24

Perfect score: 132

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Gapop 60.0 , Gapext 60.0

Searched: 1736639 seqs, 388189149 residues

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Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	132	100.0	374	14	US-10-205-194-168
2	132	100.0	385	9	US-09-925-302-624
3	132	100.0	385	10	US-09-925-302-624
4	35	26.5	35	9	US-09-864-761-44291
5	33	25.0	195	9	US-09-764-864-1190
6	8	6.1	307	16	US-10-437-963-135131
7	5.3	46	14	US-10-201-444-7	
8	7	5.3	59	16	US-10-425-115-266892
9	7	5.3	66	16	US-10-437-963-171570
10	7	5.3	71	15	US-10-424-599-264355
11	7	5.3	78	16	US-10-425-115-263100

Sequence 357584,	US-10-425-115-357584	16	87	5.3	7
Sequence 170573,	US-10-437-963-170573	16	102	5.3	7
Sequence 361810,	US-10-425-115-361810	129	129	5.3	7
Sequence 44370, A	US-10-425-114-44370	146	146	5.3	7
Sequence 56, Appl	US-10-328-675A-56	165	14	5.3	7
Sequence 52, Appl	US-10-328-675A-52	166	14	5.3	7
Sequence 2380, Ap	US-10-094-749-2380	166	14	5.3	7
Sequence 1952, Ap	US-10-264-237-1952	166	14	5.3	7
Sequence 226770,	US-10-424-599-226770	170	15	5.3	7
Sequence 147534,	US-10-437-963-147534	189	16	5.3	7
Sequence 67410, A	US-10-282-122A-67410	197	15	5.3	7
Sequence 220909,	US-10-425-115-220909	200	16	5.3	7
Sequence 40890, A	US-10-767-701-40890	216	16	5.3	7
Sequence 437, App	US-10-205-823-437	226	14	5.3	7
Sequence 1086, Ap	US-09-925-300-1086	238	9	5.3	7
Sequence 7753, Ap	US-10-739-930-7753	238	16	5.3	7
Sequence 21, Appl	US-10-770-127-21	242	16	5.3	7
Sequence 55, Appl	US-09-393-634-55	245	9	5.3	7
Sequence 55, Appl	US-09-510-332-21	245	10	5.3	7
Sequence 55, Appl	US-10-383-982-55	245	14	5.3	7
Sequence 21, Appl	US-10-364-861-55	245	15	5.3	7
Sequence 192662,	US-10-962-365-21	245	17	5.3	7
Sequence 1218, Ap	US-10-424-599-192662	267	15	5.3	7
Sequence 78, Appl	US-10-472-928-1218	302	17	5.3	7
Sequence 61658, A	US-10-926-543-78	317	17	5.3	7
Sequence 122405,	US-10-425-115-269070	348	16	5.3	7
Sequence 61118, A	US-10-282-122A-61658	359	15	5.3	7
Sequence 98, Appl	US-10-437-963-122405	371	16	5.3	7
Sequence 155, App	US-10-425-114-64118	434	15	5.3	7
Sequence 155, App	US-10-092-900A-98	518	15	5.3	7
Sequence 220226,	US-10-126-103-155	520	15	5.3	7
Sequence 16, Appl	US-10-431-096-155	523	15	5.3	7
Sequence 19, Appl	US-10-424-599-220226	567	16	5.3	7
Sequence 170375,	US-10-638-225-16	567	16	5.3	7
Sequence 73860, A	US-10-437-963-170375	611	16	5.3	7
Sequence 120133,	US-10-437-963-120133	684	15	5.3	7
Sequence 1849, Ap	US-10-282-122A-73860	691	18	5.3	7
Sequence 2368, Ap	US-10-617-320-4260	748	17	5.3	7
Sequence 157156,	US-10-732-923-1849	814	16	5.3	7
Sequence 3767, Ap	US-10-437-963-157156	817	16	5.3	7
Sequence 40, Appl	US-10-389-566-2368	1066	16	5.3	7
Sequence 40, Appl	US-10-369-493-3767	1500	15	5.3	7
Sequence 15, Appl	US-10-357-175-40	9	14	4.5	6
Sequence 3, Appli	US-10-425-115-34821	9	14	4.5	6
Sequence 1, Appli	US-10-357-720-40	17	14	4.5	6
Sequence 7, Appli	US-10-029-386-32634	17	14	4.5	6
Sequence 21, Appl	US-10-666-778-5	37	15	4.5	6
Sequence 5, Appli	US-10-424-599-207512	38	15	4.5	6
Sequence 16, Appl	US-10-685-105-16	38	16	4.5	6
Sequence 348621,	US-10-425-115-348621	39	16	4.5	6
Sequence 47125, A	US-09-864-761-47125	40	9	4.5	6
Sequence 149981,	US-10-424-599-149981	40	15	4.5	6
Sequence 23, Appl	US-10-685-105-23	41	16	4.5	6
Sequence 133, App	US-10-321-857-133	42	14	4.5	6
Sequence 133, App	US-10-318-675-133	42	14	4.5	6
Sequence 462, App	US-10-097-111-462	44	14	4.5	6
Sequence 182051,	US-10-437-963-182051	44	16	4.5	6
Sequence 180, App	US-09-974-879-180	45	15	4.5	6
Sequence 180, App	US-10-621-401-180	45	15	4.5	6
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Sequence 180, App	US-09-818-683-180	46	11	4.5	6
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Sequence 291846,	US-10-109-048-1108	46	16	4.5	6
Sequence 366211,	US-10-425-115-291846	47	16	4.5	6
Sequence 191303,	US-10-425-115-366211	47	16	4.5	6
	US-10-424-599-191303	49	15	4.5	6

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88	6	4.5	55	16	US-10-425-115-309219	Sequence 309219,	161	6	4.5	93	13	US-10-013-379-42	Sequence 42, Appl
89	6	4.5	57	16	US-10-425-115-236873	Sequence 236873,	162	6	4.5	93	15	US-10-424-599-150911	Sequence 150911,
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91	6	4.5	59	15	US-10-424-599-201490	Sequence 201490,	164	6	4.5	93	16	US-10-437-963-106822	Sequence 106822,
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93	6	4.5	60	16	US-10-425-115-228747	Sequence 228747,	166	6	4.5	94	15	US-10-424-599-190551	Sequence 190551,
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97	6	4.5	65	14	US-10-086-882-4	Sequence 4, Appli	170	6	4.5	96	16	US-10-425-115-189721	Sequence 189721,
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102	6	4.5	66	15	US-10-424-599-224581	Sequence 224581,	175	6	4.5	98	16	US-10-425-115-338617	Sequence 338617,
103	6	4.5	66	16	US-10-425-115-311508	Sequence 311508,	176	6	4.5	99	15	US-10-424-599-277703	Sequence 277703,
104	6	4.5	67	9	US-09-925-300-1005	Sequence 1005, Ap	177	6	4.5	99	15	US-10-289-762-237	Sequence 237, App
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106	6	4.5	67	16	US-10-425-115-244592	Sequence 244592,	179	6	4.5	100	15	US-10-424-599-220157	Sequence 220157,
107	6	4.5	70	15	US-10-424-599-178124	Sequence 178124,	180	6	4.5	100	15	US-10-424-599-256694	Sequence 256694,
108	6	4.5	70	15	US-10-424-599-216648	Sequence 216648,	181	6	4.5	100	15	US-10-425-115-340652	Sequence 340652,
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110	6	4.5	71	15	US-10-424-599-180886	Sequence 180886,	183	6	4.5	102	15	US-10-424-599-208588	Sequence 208588,
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116	6	4.5	74	14	US-10-252-945-111	Sequence 111, App	189	6	4.5	105	11	US-09-833-245-1824	Sequence 1824, Ap
117	6	4.5	74	16	US-10-767-701-54400	Sequence 54400, A	190	6	4.5	105	16	US-10-425-115-354491	Sequence 354491,
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119	6	4.5	75	15	US-10-104-755-12	Sequence 12, Appl	192	6	4.5	106	14	US-10-213-512-208	Sequence 208, App
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125	6	4.5	77	14	US-10-083-357-1240	Sequence 1240, Ap	198	6	4.5	109	14	US-10-230-331-42	Sequence 42, Appl
126	6	4.5	77	15	US-10-375-209A-14	Sequence 14, Appl	199	6	4.5	109	15	US-10-424-599-213081	Sequence 213081,
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136	6	4.5	80	15	US-10-057-475B-1854	Sequence 1854, Ap	209	6	4.5	112	15	US-10-424-599-159487	Sequence 159487,
137	6	4.5	80	15	US-10-154-884B-1854	Sequence 1854, Ap	210	6	4.5	112	15	US-10-424-599-203048	Sequence 203048,
138	6	4.5	80	15	US-10-425-114-42385	Sequence 42385, A	211	6	4.5	112	15	US-10-424-599-203049	Sequence 203049,
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147	6	4.5	84	14	US-10-092-154-771	Sequence 771, App	220	6	4.5	112	16	US-10-425-115-350383	Sequence 350383,
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265	6	4.5	131	15	US-10-424-599-209370	Sequence 209370,	338	6	4.5	177	14	US-10-205-428-440	Sequence 440, App
266	6	4.5	132	15	US-10-424-599-280783	Sequence 280783,	339	6	4.5	177	16	US-10-437-963-160181	Sequence 160181,
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274	6	4.5	136	14	US-10-004-860-1009	Sequence 1009, Ap	347	6	4.5	180	16	US-10-282-122A-54695	Sequence 54695, A
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283	6	4.5	140	15	US-10-424-599-164843	Sequence 164843,	356	6	4.5	192	16	US-10-425-115-270897	Sequence 270897,
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379	6	4.5	203	16	US-10-425-114-223267	Sequence 223267, A	452	6	4.5	233	16	US-10-795-157-6	Sequence 6, Appli
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392	6	4.5	211	15	US-10-425-114-46315	Sequence 46315, A	465	6	4.5	244	17	US-10-899-557-41	Sequence 41, Appl
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403	6	4.5	217	16	US-10-369-493-319	Sequence 319, App	476	6	4.5	252	14	US-10-017-161-76	Sequence 76, Appl
404	6	4.5	217	16	US-10-437-963-139073	Sequence 139073, A	477	6	4.5	254	14	US-10-292-798-68	Sequence 68, Appl
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408	6	4.5	219	11	US-09-833-245-1130	Sequence 1130, Ap	481	6	4.5	257	16	US-10-617-320-3792	Sequence 3792, Ap
409	6	4.5	219	16	US-10-437-963-149216	Sequence 149216, A	482	6	4.5	258	15	US-10-187-975-68	Sequence 53015, A
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436	6	4.5	225	9	US-09-764-898-227	Sequence 227, App	509	6	4.5	287	15	US-10-369-493-20892	Sequence 20892, A
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438	6	4.5	225	15	US-10-425-114-38466	Sequence 38466, A	511	6	4.5	290	15	US-10-187-975-70	Sequence 70, Appl
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525	6	4.5	296	15	US-10-424-599-193973	Sequence 193973, A	598	17	US-10-485-710-107	Sequence 107, App
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529	6	4.5	298	15	US-10-374-780A-2478	Sequence 2478, App	602	15	US-10-369-493-8062	Sequence 8062, App
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548	6	4.5	309	15	US-10-292-798-196	Sequence 490, App	621	6	US-10-369-493-1424	Sequence 1424, App
549	6	4.5	309	15	US-10-343-650A-490	Sequence 9, Appli	622	6	US-10-087-192-120	Sequence 120, App
550	6	4.5	309	16	US-10-473-518-9	Sequence 470, App	623	6	US-10-369-493-3724	Sequence 3724, App
551	6	4.5	312	14	US-10-017-161-470	Sequence 230, App	624	6	US-10-437-963-132724	Sequence 132724, App
552	6	4.5	312	15	US-10-387-629-230	Sequence 420, App	625	6	US-10-472-928-2788	Sequence 2788, App
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565	6	4.5	318	14	US-10-001-254-18	Sequence 18, Appl	638	6	US-10-004-860-1008	Sequence 1008, App
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569	6	4.5	319	10	US-09-925-302-758	Sequence 758, App	642	6	US-10-369-493-6752	Sequence 6752, App
570	6	4.5	319	15	US-10-424-599-142910	Sequence 142910, A	643	6	US-10-739-930-10454	Sequence 10454, A
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ALIGNMENTS

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; Sequence 168, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 168
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Speckle-type protein
US-10-205-194-168

Query Match 100.0%; Score 132; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.7e-125;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 624, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-624
Query Match 100.0%; Score 132; DB 9; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-125;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 624, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
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US-09-925-302-624

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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44291
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; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006487.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.79
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EST HUMAN HIT: BE876686.1, EVALUE 3.00e-14
; OTHER INFORMATION: SWISSPROT HIT: O43791, EVALUE 2.00e-15
US-09-864-761-44291

Query Match      26.5%; Score 35; DB 9; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 SQRAYRFVQGDWGFKKFIRRDFLDDEANGLLPD 121
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Db 1 SQRAYRFVQGDWGFKKFIRRDFLDDEANGLLPD 35
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RESULT 5
US-09-764-864-1190
; Sequence 1190, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1190
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (171)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1190

Query Match      25.0%; Score 33; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 5.6e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 GFKKFIRRDFLDDEANGLLPDKLTLCFCEVSVV 132
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Db 3 GFKKFIRRDFLDDEANGLLPDKLTLCFCEVSVV 35
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RESULT 6
US-10-437-963-135131
; Sequence 135131, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
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nothing before 2000

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135131
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_36836C.1.pep
US-10-437-963-135131

Query Match 6.1%; Score 8; DB 16; Length 307;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 LDEANGLL 118
Db 68 LDEANGLL 75

RESULT 7
US-10-201-444-7
; Sequence 7, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 6375377
; CURRENT APPLICATION NUMBER: US/10/201.444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861.476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-7

Query Match 5.3%; Score 7; DB 14; Length 46;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 DFLDLEA 114
Db 29 DFLDLEA 35

RESULT 8
US-10-425-115-266892
; Sequence 266892, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 266892
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_175007C.1.pep
US-10-425-115-266892

Query Match 5.3%; Score 7; DB 16; Length 59;
Best Local Similarity 100.0%; Pred. No. 41;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 72 FSLINAK 78
Db 9 FSLINAK 15

RESULT 9
US-10-437-963-171570
; Sequence 171570, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437.963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 171570
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_6978C.1.pep
US-10-437-963-171570

Query Match 5.3%; Score 7; DB 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 LSLYLLL 58
Db 13 LSLYLLL 19

RESULT 10
US-10-424-599-264355
; Sequence 264355, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424.599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 264355
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80733C.1.pep
US-10-424-599-264355

Query Match 5.3%; Score 7; DB 15; Length 71;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 SLYLVLV 59
Db 13 SLYLVLV 19

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RESULT 11
US-10-425-115-263100
; Sequence 263100, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 269326
; SEQ ID NO 263100
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_17155C.1.pep
US-10-425-115-263100

Query Match          5.3%; Score 7; DB 16; Length 78;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 YLSLYLL 57
Db 54 YLSLYLL 60

RESULT 12
US-10-425-115-357584
; Sequence 357584, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 357584
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_89285C.1.pep
US-10-425-115-357584

Query Match          5.3%; Score 7; DB 16; Length 87;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 KSSTFSS 27
Db 78 KSSTFSS 84

RESULT 13
US-10-437-963-170573
; Sequence 170573, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 170573
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68887C.1.pep
US-10-437-963-170573

Query Match          5.3%; Score 7; DB 16; Length 102;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 BETKAME 86
Db 33 BETKAME 39

RESULT 14
US-10-425-115-361810
; Sequence 361810, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 361810
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_93147C.1.pep
US-10-425-115-361810

Query Match          5.3%; Score 7; DB 16; Length 129;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 MGEVIKS 22
Db 69 MGEVIKS 75

RESULT 15
US-10-425-114-44370
; Sequence 44370, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 44370

; LENGTH: 146

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 701169325_FLI.pep

US-10-425-114-44370

Query Match 5.3%; Score 7; DB 15; Length 146;
Best Local Similarity 100.0%; Pred.No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 LLDEANG 116

Db 66 LLDEANG 72

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:38:46 ; Search time 25.3929 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7	5.2	133	4	US-09-270-767-35069, A
2	7	5.2	133	4	US-09-270-767-50286, A
3	7	5.2	138	4	US-09-902-540-13575, A
4	7	5.2	145	3	US-09-134-001C-5194, A
5	7	5.2	411	4	US-08-887-534A-80, A
6	7	5.2	411	4	US-09-527-431-80, A
7	7	5.2	411	4	US-09-446-861-80, A
8	7	5.2	548	4	US-09-252-991A-20793, A
9	7	5.2	651	4	US-09-932-678-2, A
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11	6	4.4	39	1	US-08-428-488-13, A
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13	6	4.4	52	4	US-09-096-724B-32, A
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15	6	4.4	60	4	US-09-248-796A-24792, A
16	6	4.4	63	4	US-09-480-297A-30, A
17	6	4.4	69	4	US-09-328-352-4927, A
18	6	4.4	77	4	US-09-513-999C-6277, A
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22	6	4.4	112	4	US-09-513-999C-4379, A
23	6	4.4	132	4	US-09-513-999C-5589, A
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26	6	4.4	140	4	US-09-252-991A-16605, A
27	6	4.4	141	4	US-09-621-976-6981, A

28	6	4.4	141	4	US-09-621-976-6982, A
29	6	4.4	141	4	US-09-513-999C-7895, A
30	6	4.4	142	4	US-09-216-393B-24, A
31	6	4.4	166	4	US-09-621-976-5267, A
32	6	4.4	171	4	US-09-902-540-16814, A
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35	6	4.4	182	3	US-09-134-001C-3742, A
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37	6	4.4	208	4	US-09-328-352-4746, A
38	6	4.4	209	4	US-09-096-724B-8, A
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55	6	4.4	276	4	US-09-252-991A-18006, A
56	6	4.4	276	4	US-09-489-039A-9409, A
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58	6	4.4	290	4	US-09-270-767-54448, A
59	6	4.4	291	4	US-09-252-991A-28755, A
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63	6	4.4	302	4	US-09-489-039A-8608, A
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65	6	4.4	306	1	US-08-217-327-6, A
66	6	4.4	310	4	US-09-598-747-27, A
67	6	4.4	311	4	US-09-489-039A-12640, A
68	6	4.4	312	4	US-09-949-016-8777, A
69	6	4.4	314	4	US-09-902-540-10356, A
70	6	4.4	315	4	US-09-252-991A-31850, A
71	6	4.4	315	4	US-09-710-279-2100, A
72	6	4.4	319	4	US-09-107-532A-5122, A
73	6	4.4	321	4	US-09-540-236-2542, A
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82	6	4.4	332	3	US-09-540-014-9, A
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Sequence 6982, Ap
Sequence 7895, Ap
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Sequence 5267, Ap
Sequence 16814, A
Sequence 5373, Ap
Sequence 86, Appl
Sequence 7611, Ap
Sequence 4746, Ap
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Sequence 24, Appl
Sequence 18224, A
Sequence 39, Appl
Sequence 128, App
Sequence 17464, A
Sequence 38019, A
Sequence 5336, A
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Sequence 327, App
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Sequence 5999, Ap
Sequence 5, Appl
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Sequence 9, Appl
Sequence 1049, Ap
Sequence 588, App
Sequence 2, Appl
Sequence 16933, A
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121	6	4.4	489	4	US-09-252-991A-18577	Sequence 18577, A	194	6	4.4	744	4	US-09-252-991A-28519	Sequence 28519, A
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126	6	4.4	492	4	US-09-986-552-19	Sequence 19, Appl	199	6	4.4	832	4	US-09-949-016-7810	Sequence 7810, Ap
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138	6	4.4	515	4	US-09-635-872A-6	Sequence 6, Appli	211	6	4.4	946	4	US-09-657-931A-10	Sequence 10, Appl
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144	6	4.4	515	4	US-10-023-884-18	Sequence 18, Appl	217	6	4.4	1036	4	US-09-398-239-5	Sequence 5, Appli
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150	6	4.4	527	4	US-09-252-991A-17196	Sequence 17196, A	223	6	4.4	1272	4	US-09-949-016-7472	Sequence 7472, Ap
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166	6	4.4	570	4	US-09-949-016-8263	Sequence 8263, Ap	239	6	4.4	1580	3	US-09-208-716-1	Sequence 1, Appli
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265	6	4.4	2291	4	US-09-252-991A-21854	Sequence 21854, A	338	5	3.7	23	3	US-09-070-291-6	Sequence 6, Appli
266	6	4.4	2314	3	US-08-268-347-49	Sequence 49, Appli	339	5	3.7	23	4	US-09-790-497A-114	Sequence 114, App
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316	5	3.7	20	2	US-08-433-133-96	Sequence 96, Appli	389	5	3.7	26	4	US-09-136-159A-119	Sequence 119, App
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318	5	3.7	21	4	US-09-500-124-121	Sequence 121, App	391	5	3.7	26	4	US-09-576-824A-115	Sequence 115, App
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570	5	3.7	79	3	US-08-993-254-3	Sequence 3, Appl	643	5	3.7	92	3	US-08-479-603-23	Sequence 23, Appl
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578	5	3.7	80	1	US-08-487-174-41	Sequence 41, Appl	651	5	3.7	92	4	US-09-467-638-9	Sequence 9, Appl
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593	5	3.7	81	4	US-09-107-532A-5379	Sequence 5379, Ap	666	5	3.7	93	4	US-09-266-965-117	Sequence 117, App
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598	5	3.7	82	4	US-09-513-999C-7239	Sequence 7239, Ap	671	5	3.7	93	4	US-09-270-767-54320	Sequence 54320, A
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689	5	3.7	96	3	US-09-479-729B-2	Sequence 2, Appli	762	5	3.7	104	4	US-08-456-033-26	Sequence 27, Appli
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705	5	3.7	97	4	US-09-513-999C-4277	Sequence 4277, Ap	778	5	3.7	106	4	US-09-270-767-58597	Sequence 58597, A
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716	5	3.7	99	4	US-09-640-211A-2111	Sequence 2111, Ap	789	5	3.7	109	2	US-08-343-443B-6	Sequence 6, Appli
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740	5	3.7	103	4	US-09-270-767-48516	Sequence 48516, A	813	5	3.7	116	3	US-09-211-290-5	Sequence 5, Appli
741	5	3.7	103	4	US-09-220-407-164	Sequence 164, App	814	5	3.7	116	3	US-09-030-613-5	Sequence 5, Appli
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756	5	3.7	104	3	US-08-445-467-26	Sequence 26, Appli	829	5	3.7	119	2	US-08-491-835-16	Sequence 16, Appli
757	5	3.7	104	3	US-08-480-515A-26	Sequence 26, Appli	830	5	3.7	119	3	US-09-153-733A-18	Sequence 18, Appli

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848	5	3.7	120	3	US-09-145-060-20	Sequence 20, Appl	921	136	3	US-08-894-998A-40	Sequence 40, Appl
849	5	3.7	120	4	US-09-378-238-34	Sequence 34, Appl	922	136	4	US-09-134-000C-6410	Sequence 6410, Ap
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858	5	3.7	120	5	PCT-US94-07762-14	Sequence 14, Appl	931	137	3	US-09-328-352-5960	Sequence 5960, Ap
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879	5	3.7	125	4	US-09-615-192A-321	Sequence 321, App	952	141	4	US-09-270-767-61539	Sequence 61539, A
880	5	3.7	125	4	US-09-732-210-72	Sequence 72, Appl	953	141	4	US-09-252-991A-19283	Sequence 19283, A
881	5	3.7	125	4	US-09-489-039A-11259	Sequence 11259, A	954	142	4	US-09-732-210-379	Sequence 379, App
882	5	3.7	125	4	US-09-270-767-39908	Sequence 39908, A	955	142	4	US-09-543-681A-4478	Sequence 4478, Ap
883	5	3.7	125	4	US-09-270-767-54125	Sequence 54125, A	956	142	4	US-09-621-976-6716	Sequence 6716, Ap
884	5	3.7	126	4	US-09-252-991A-16596	Sequence 16596, A	957	142	4	US-09-540-236-2489	Sequence 2489, Ap
885	5	3.7	126	4	US-09-621-976-4120	Sequence 4120, Ap	958	142	4	US-09-583-110-3744	Sequence 3744, Ap
886	5	3.7	126	4	US-09-898-659-37	Sequence 37, Appl	959	142	4	US-09-248-796A-20953	Sequence 20953, A
887	5	3.7	126	4	US-09-107-433-3836	Sequence 3836, Ap	960	142	4	US-09-252-991A-21044	Sequence 21044, A
888	5	3.7	127	2	US-08-853-659A-57	Sequence 57, Appl	961	143	4	US-09-252-991A-32948	Sequence 32948, A
889	5	3.7	127	4	US-09-489-039A-8547	Sequence 8547, Ap	962	143	4	US-09-270-767-37046	Sequence 37046, A
890	5	3.7	127	4	US-09-270-767-32286	Sequence 32286, A	963	143	4	US-09-270-767-38860	Sequence 38860, A
891	5	3.7	127	4	US-09-902-540-10294	Sequence 10294, A	964	143	4	US-09-270-767-52263	Sequence 52263, A
892	5	3.7	128	4	US-09-711-164-337	Sequence 337, App	965	143	4	US-09-270-767-54077	Sequence 54077, A
893	5	3.7	128	4	US-09-583-110-5238	Sequence 5238, Ap	966	143	4	US-09-082-920-6	Sequence 6, Appli
894	5	3.7	129	4	US-09-732-210-63	Sequence 63, Appl	967	144	3	US-09-107-532A-4029	Sequence 4029, Ap
895	5	3.7	129	4	US-09-489-039A-8776	Sequence 8776, Ap	968	144	4	US-09-543-681A-6998	Sequence 6998, Ap
896	5	3.7	129	4	US-10-029-180-90	Sequence 90, Appl	969	144	4	US-09-621-976-5094	Sequence 5094, Ap
897	5	3.7	130	4	US-09-252-991A-23006	Sequence 23006, A	970	144	4	US-09-270-767-48278	Sequence 48278, A
898	5	3.7	131	4	US-09-631-594-78	Sequence 78, Appl	971	144	4	US-09-248-796A-20083	Sequence 20083, A
899	5	3.7	132	4	US-09-107-532A-7283	Sequence 7283, Ap	972	145	2	US-08-406-057-8	Sequence 8, Appli
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902	5	3.7	133	1	US-08-346-611-2	Sequence 2, Appli	975				
903	5	3.7	133	2	US-08-794-494-2	Sequence 2, Appli	976				

977 5 3.7 145 3 US-08-946-329A-55 Sequence 55, Appl
978 5 3.7 145 3 US-08-946-329A-56 Sequence 56, Appl
979 5 3.7 145 3 US-09-030-613-9 Sequence 9, Appl
980 5 3.7 145 3 US-08-958-316-8 Sequence 8, Appl
981 5 3.7 145 3 US-09-451-905-9 Sequence 9, Appl
982 5 3.7 145 4 US-09-252-991A-19228 Sequence 19228, A
983 5 3.7 146 3 US-09-105-343A-6 Sequence 6, Appl
984 5 3.7 146 4 US-09-252-991A-20372 Sequence 20372, A
985 5 3.7 146 4 US-09-252-991A-26454 Sequence 26454, A
986 5 3.7 146 4 US-09-543-681A-5030 Sequence 5030, Ap
987 5 3.7 146 4 US-09-640-211A-680 Sequence 680, App
988 5 3.7 146 4 US-09-902-540-12616 Sequence 12616, A
989 5 3.7 147 2 US-08-824-405-12 Sequence 12, Appl
990 5 3.7 147 4 US-09-621-976-4802 Sequence 4802, Ap
991 5 3.7 147 4 US-09-270-767-32088 Sequence 32088, A
992 5 3.7 147 4 US-09-270-767-58356 Sequence 58356, A
993 5 3.7 147 4 US-09-248-796A-20089 Sequence 20089, A
994 5 3.7 147 4 US-09-809-665A-56 Sequence 56, Appl
995 5 3.7 148 4 US-09-732-210-328 Sequence 328, App
996 5 3.7 148 4 US-09-540-236-2105 Sequence 2105, Ap
997 5 3.7 148 4 US-09-640-211A-1139 Sequence 1139, Ap
998 5 3.7 150 4 US-09-732-210-329 Sequence 329, App
999 5 3.7 150 4 US-09-270-767-61388 Sequence 61388, A
1000 5 3.7 151 4 US-09-732-210-1353 Sequence 1353, Ap

ALIGNMENTS

RESULT 1
US-09-270-767-35069
; Sequence 35069, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35069
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-35069

Query Match 5.2%; Score 7; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FVLENFS 17
Db 21 FVLENFS 27

RESULT 2
US-09-270-767-50286
; Sequence 50286, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50286
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-50286

Query Match 5.2%; Score 7; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FVLENFS 17
Db 21 FVLENFS 27

RESULT 3
US-09-902-540-13575
; Sequence 13575, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13575
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13575

Query Match 5.2%; Score 7; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 AGLPETS 69
Db 27 AGLPETS 33

RESULT 4
US-09-134-001C-5194
; Sequence 5194, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GFC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5194
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5194

Query Match 5.2%; Score 7; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
Db 21 DSATFVL 27

RESULT 5

US-08-887-534A-80
; Sequence 80, Application US/08887534A
; Patent No. 6455323
; GENERAL INFORMATION:
; APPLICANT: Holden, David W.
; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,534A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/33996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-887-534A-80

Query Match 5.2%; Score 7; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
| | | | |
Db 286 DSATFVL 292

RESULT 6
US-09-527-431-80
; Sequence 80, Application US/09527431
; Patent No. 6485899
; GENERAL INFORMATION:
; APPLICANT: Holden, David W.
; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/527,431
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,534
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/33996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-527-431-80

Query Match 5.2%; Score 7; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
| | | | |
Db 286 DSATFVL 292

RESULT 7
US-09-446-861-80
; Sequence 80, Application US/09446861
; Patent No. 6740485
; GENERAL INFORMATION:
; APPLICANT: Holden, David W.
; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Li-Hsien Rin-Laures, M.D.
; STREET: 6300 Sears Tower 233 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/446,861
; FILING DATE: 22-Mar-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Li-Hsien Rin-Laures, M.D.
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/6314.PCP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-446-861-80

Query Match 5.2%; Score 7; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
| | | | |

Db 286 DSATFVL 292

RESULT 8

US-09-252-991A-20793
; Sequence 20793, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20793
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20793

Query Match 5.2%; Score 7; DB 4; Length 548;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 QQRADPV 26

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Db 247 QQRADPV 253

RESULT 9

US-09-932-678-2
; Sequence 2, Application US/09932678
; Patent No. 6825034
; GENERAL INFORMATION:
; APPLICANT: Reeder, Ronald H.
; APPLICANT: Moorefield, Beth
; APPLICANT: Greene, Elizabeth A.
; TITLE OF INVENTION: HUMAN RN3 AND COMPOSITIONS AND METHODS RELATING
; FILE REFERENCE: 14538A-005810US
; CURRENT APPLICATION NUMBER: US/09/932,678
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/225,893
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-932-678-2

Query Match 5.2%; Score 7; DB 4; Length 651;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 PQNDTVI 128

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Db 614 PQNDTVI 620

RESULT 10

US-09-902-540-16517
; Sequence 16517, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16517
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16517

Query Match 4.4%; Score 6; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 LSVFLE 60

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Db 20 LSVFLE 25

RESULT 11

US-08-428-488-13
; Sequence 13, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P. O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = H-Ser."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 39
; OTHER INFORMATION: /note= "Position 39 = Phe-OH."
; FEATURE:
; NAME/KEY: Modified-site

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; LOCATION: 30
; OTHER INFORMATION: /note= "Position 30 = Glu-NH2."
US-08-428-488-13

Query Match          4.4%; Score 6; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 KVPDGG 46
Db 21 KVPDGG 26

RESULT 12
US-08-960-022-12
; Sequence 12, Application US/08960022
; Patent No. 5976837
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,022
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-960-022-12

Query Match          4.4%; Score 6; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 SVFLEL 61
Db 26 SVFLEL 31

RESULT 13
US-09-096-724B-32
; Sequence 32, Application US/09096724B
; Patent No. 6548290
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; GENERAL INFORMATION:
; APPLICANT: McGarity, Thomas J.
; APPLICANT: Kroll, Kristen
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Geminin Gene and Protein
; FILE REFERENCE: 0725.1055-001
; CURRENT APPLICATION NUMBER: US/09/096,724B
; CURRENT FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/085,371
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 52
; TYPE: PRT
; ORGANISM: human
US-09-096-724B-32

Query Match          4.4%; Score 6; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 ELSAGL 65
Db 16 ELSAGL 21

RESULT 14
US-09-621-976-4130
; Sequence 4130, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4130
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41..-1
US-09-621-976-4130

Query Match          4.4%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 NEGYLN 121
Db 45 NEGYLN 50

RESULT 15
US-09-248-796A-24792
; Sequence 24792, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
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; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24792
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24792

Query Match      4.4%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      86 TKNIIR 91
      |||||
Db      47 TKNIIR 52
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Search completed: July 20, 2005, 20:53:58
Job time : 27.3929 secs

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:52:32 ; Search time 85.8214 Seconds
(without alignments)
610.633 Million cell updates/sec

Title: US-09-706-325-25

Perfect score: 135

Sequence: 1 ELVPSYDSATFVLENFSTLR.....NEGYNPQNDTVILRFQVRS 135

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1736639 seqs, 388188149 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	135	100.0	979	16	US-10-473-127-425
6	135	100.0	979	16	US-10-473-127-426
7	135	100.0	979	16	US-10-473-127-427
8	135	100.0	979	16	US-10-473-127-432
9	135	100.0	1016	16	US-10-473-127-430
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11	9	6.7	55	10	US-09-992-238-33

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16	6.7	398	15	US-10-436-715-16	Sequence 16, Appl
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21	6.7	448	16	US-10-712-615-42	Sequence 42, Appl
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235	6	4.4	166	15	US-10-424-599-322795	Sequence 322795, App	308	6	4.4	254	16	US-10-408-768A-1182	Sequence 1182, App
236	6	4.4	166	17	US-10-643-836-3225	Sequence 3225, App	309	6	4.4	254	16	US-10-425-115-254726	Sequence 254726, App
237	6	4.4	169	15	US-10-424-599-283105	Sequence 283105, App	310	6	4.4	255	16	US-10-425-115-304375	Sequence 304375, App
238	6	4.4	171	14	US-10-156-761-9002	Sequence 9002, App	311	6	4.4	258	16	US-10-425-115-360298	Sequence 360298, App
239	6	4.4	172	16	US-10-425-115-278321	Sequence 278321, App	312	6	4.4	258	16	US-10-425-115-361426	Sequence 361426, App
240	6	4.4	172	16	US-10-425-115-319910	Sequence 319910, App	313	6	4.4	260	15	US-10-424-599-271735	Sequence 271735, App
241	6	4.4	176	15	US-10-243-552-465	Sequence 465, App	314	6	4.4	260	15	US-10-425-114-40642	Sequence 40642, A
242	6	4.4	177	15	US-10-424-599-218587	Sequence 218587, App	315	6	4.4	262	14	US-10-050-704-159	Sequence 159, App
243	6	4.4	177	15	US-10-424-599-257776	Sequence 257776, App	316	6	4.4	262	14	US-10-335-977-6501	Sequence 6501, App
244	6	4.4	179	16	US-10-767-701-40128	Sequence 40128, A	317	6	4.4	262	16	US-10-798-512-159	Sequence 159, App
245	6	4.4	180	16	US-10-467-534-87	Sequence 87, App	318	6	4.4	263	15	US-10-282-122A-53892	Sequence 53892, A
246	6	4.4	180	16	US-10-699-035A-2	Sequence 2, Appli	319	6	4.4	274	15	US-10-282-122A-56737	Sequence 56737, A
247	6	4.4	182	16	US-10-724-972A-4808	Sequence 4808, App	320	6	4.4	275	14	US-10-274-409-5	Sequence 5, Appli
248	6	4.4	184	15	US-10-214-529-30	Sequence 30, Appl	321	6	4.4	275	14	US-10-369-493-15465	Sequence 15465, A
249	6	4.4	184	16	US-10-767-701-41064	Sequence 41064, A	322	6	4.4	275	15	US-10-369-493-15834	Sequence 15834, A
250	6	4.4	185	9	US-09-925-298-439	Sequence 439, App	323	6	4.4	275	17	US-10-932-135-5	Sequence 5, Appli
251	6	4.4	185	14	US-10-149-819-18	Sequence 18, App	324	6	4.4	277	16	US-10-437-963-165590	Sequence 165590, A
252	6	4.4	185	14	US-10-102-806-439	Sequence 439, App	325	6	4.4	278	16	US-10-767-701-39033	Sequence 39033, A
253	6	4.4	186	14	US-10-097-065-341	Sequence 341, App	326	6	4.4	281	16	US-10-767-701-39700	Sequence 39700, A
254	6	4.4	186	15	US-10-372-876-341	Sequence 341, App	327	6	4.4	290	15	US-10-369-493-12659	Sequence 12659, A
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257	6	4.4	188	16	US-10-425-115-205993	Sequence 205993, App	330	6	4.4	293	16	US-10-767-701-44064	Sequence 44064, A
258	6	4.4	189	15	US-10-424-599-148735	Sequence 148735, App	331	6	4.4	294	16	US-10-437-963-141196	Sequence 141196, A
259	6	4.4	189	15	US-10-276-774-2120	Sequence 2120, App	332	6	4.4	294	17	US-10-732-923-20178	Sequence 20178, A
260	6	4.4	189	16	US-10-425-115-205277	Sequence 205277, App	333	6	4.4	295	15	US-10-289-762-11233	Sequence 1123, App
261	6	4.4	193	15	US-10-364-237-2190	Sequence 2190, App	334	6	4.4	295	14	US-10-425-114-40997	Sequence 40997, A
262	6	4.4	193	15	US-10-335-977-5167	Sequence 5167, App	335	6	4.4	296	14	US-10-287-274-327	Sequence 327, App
263	6	4.4	195	14	US-10-424-599-173417	Sequence 173417, App	336	6	4.4	297	9	US-09-815-242-5149	Sequence 5149, App
264	6	4.4	196	14	US-10-017-161-1340	Sequence 1340, App	337	6	4.4	297	15	US-10-282-122A-43496	Sequence 43496, A
265	6	4.4	196	15	US-10-292-738-1100	Sequence 1100, App	338	6	4.4	302	16	US-10-767-701-38529	Sequence 38529, A
266	6	4.4	200	14	US-10-178-055-4	Sequence 4, Appli	339	6	4.4	304	16	US-10-767-701-41568	Sequence 41568, A
267	6	4.4	200	16	US-10-425-115-325501	Sequence 325501, App	340	6	4.4	305	14	US-10-267-989-35	Sequence 35, Appl
268	6	4.4	205	15	US-10-424-599-273598	Sequence 273598, App	341	6	4.4	305	14	US-10-267-989-37	Sequence 37, Appl
269	6	4.4	209	14	US-10-178-055-2	Sequence 2, Appli	342	6	4.4	305	16	US-10-482-793-21	Sequence 21, Appl
270	6	4.4	209	16	US-10-733-878-427	Sequence 427, App	343	6	4.4	307	15	US-10-369-493-22522	Sequence 22522, A
271	6	4.4	211	16	US-10-767-701-51745	Sequence 51745, A	344	6	4.4	307	17	US-10-732-923-19469	Sequence 19469, A
272	6	4.4	213	15	US-10-424-599-194344	Sequence 194344, App	345	6	4.4	307	17	US-10-732-923-19270	Sequence 19270, A
273	6	4.4	213	16	US-10-425-115-275921	Sequence 275921, App	346	6	4.4	309	14	US-10-306-762-166	Sequence 166, App
274	6	4.4	214	16	US-10-437-963-157148	Sequence 157148, App	347	6	4.4	310	14	US-10-306-292-27	Sequence 27, Appl
275	6	4.4	214	16	US-10-425-115-275920	Sequence 275920, App	348	6	4.4	310	16	US-10-437-963-124167	Sequence 124167, App
276	6	4.4	215	9	US-09-789-561-85	Sequence 85, Appl	349	6	4.4	311	16	US-10-767-701-44866	Sequence 44866, A
277	6	4.4	215	11	US-09-833-245-2096	Sequence 2096, App	350	6	4.4	313	9	US-09-895-913A-68	Sequence 68, Appl
278	6	4.4	215	15	US-10-335-977-8658	Sequence 8658, App	351	6	4.4	313	15	US-10-369-493-17325	Sequence 17325, A
279	6	4.4	215	17	US-10-883-936-85	Sequence 85, Appl	352	6	4.4	313	15	US-10-282-122A-60596	Sequence 60596, A
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281	6	4.4	216	15	US-10-407-079-106	Sequence 106, App	354	6	4.4	313	16	US-10-437-963-161595	Sequence 161595, A
282	6	4.4	218	18	US-10-485-986-45	Sequence 45, Appl	355	6	4.4	314	15	US-10-425-114-69035	Sequence 69035, A
283	6	4.4	219	16	US-10-437-963-139338	Sequence 139338, App	356	6	4.4	314	16	US-10-767-701-39754	Sequence 39754, A
284	6	4.4	224	14	US-10-156-761-9369	Sequence 9369, App	357	6	4.4	318	14	US-10-156-761-12913	Sequence 12913, A
285	6	4.4	224	15	US-10-425-115-270881	Sequence 270881, App	358	6	4.4	324	18	US-10-724-972A-5146	Sequence 5146, App
286	6	4.4	225	16	US-10-424-599-203025	Sequence 203025, App	359	6	4.4	326	9	US-09-337-946A-22	Sequence 22, Appl
287	6	4.4	226	9	US-09-789-561-165	Sequence 165, App	360	6	4.4	326	14	US-10-226-007-27	Sequence 27, Appl
288	6	4.4	226	15	US-10-424-599-203023	Sequence 203023, App	361	6	4.4	326	14	US-10-156-761-13931	Sequence 13931, A
289	6	4.4	226	17	US-10-883-936-165	Sequence 165, App	362	6	4.4	326	14	US-10-224-999A-3460	Sequence 3460, App
290	6	4.4	227	15	US-10-424-599-255626	Sequence 255626, App	363	6	4.4	326	15	US-10-353-856-12	Sequence 12, Appl
291	6	4.4	227	16	US-10-425-115-364620	Sequence 364620, App	364	6	4.4	326	15	US-10-353-856-30	Sequence 30, Appl
292	6	4.4	230	17	US-10-732-923-15604	Sequence 15604, A	365	6	4.4	326	15	US-10-353-856-40	Sequence 40, Appl
293	6	4.4	232	15	US-10-282-122A-67975	Sequence 67975, A	366	6	4.4	326	15	US-10-384-976-22	Sequence 22, Appl
294	6	4.4	233	15	US-10-282-122A-65840	Sequence 65840, A	367	6	4.4	326	18	US-10-696-633-22	Sequence 22, Appl
295	6	4.4	239	16	US-10-425-115-261464	Sequence 261464, App	368	6	4.4	329	16	US-10-482-793-23	Sequence 23, Appl
296	6	4.4	240	16	US-10-437-963-186237	Sequence 186237, App	369	6	4.4	330	16	US-10-425-115-256714	Sequence 256714, App
297	6	4.4	241	9	US-09-925-301-1105	Sequence 1105, App	370	6	4.4	331	14	US-10-194-885-10	Sequence 10, Appl
298	6	4.4	241	15	US-10-282-122A-71867	Sequence 71867, A	371	6	4.4	331	16	US-10-425-115-263429	Sequence 263429, App
299	6	4.4	241	17	US-10-732-923-1916	Sequence 1916, App	372	6	4.4	332	14	US-10-091-841-9	Sequence 9, Appli
300	6	4.4	242	9	US-09-789-561-159	Sequence 159, App	373	6	4.4	332	15	US-10-425-114-47369	Sequence 47369, A
301	6	4.4	242	14	US-10-156-761-7678	Sequence 7678, App	374	6	4.4	333	15	US-10-282-122A-54905	Sequence 54905, A
302	6	4.4	242	17	US-10-883-936-159	Sequence 159, App	375	6	4.4	333	15	US-10-425-114-42556	Sequence 42556, A
303	6	4.4	244	16	US-10-437-963-175678	Sequence 175678, App	376	6	4.4	333	15	US-10-425-114-58732	Sequence 58732, A

377	6	4.4	334	15	US-10-282-122A-67021	Sequence 67021, A	450	6	4.4	418	15	US-10-369-493-17809	Sequence 17809, A
378	6	4.4	334	15	US-10-425-114-42742	Sequence 42742, A	451	6	4.4	418	16	US-10-699-035A-6	Sequence 6, Appli
379	6	4.4	342	15	US-10-107-431-63	Sequence 63, Appl	452	6	4.4	418	16	US-10-699-035A-20	Sequence 20, Appl
380	6	4.4	342	15	US-10-084-846A-88	Sequence 88, Appl	453	6	4.4	420	10	US-09-972-546-2	Sequence 2, Appli
381	6	4.4	342	15	US-10-424-599-159871	Sequence 159871, A	454	6	4.4	420	17	US-10-735-256-2	Sequence 2, Appli
382	6	4.4	343	15	US-10-282-122A-60799	Sequence 60799, A	455	6	4.4	420	17	US-10-369-493-3861	Sequence 3861, Ap
383	6	4.4	343	15	US-10-335-977-6502	Sequence 6502, Ap	456	6	4.4	427	15	US-10-369-493-9726	Sequence 9726, Ap
384	6	4.4	344	15	US-10-282-122A-66172	Sequence 66172, A	457	6	4.4	427	15	US-10-104-047-3317	Sequence 3317, Ap
385	6	4.4	344	15	US-10-282-122A-69673	Sequence 69673, A	458	6	4.4	428	15	US-10-282-122A-61465	Sequence 61465, A
386	6	4.4	344	15	US-10-369-493-1835	Sequence 1835, Ap	459	6	4.4	431	14	US-10-156-761-13184	Sequence 13184, A
387	6	4.4	346	9	US-09-829-482-2	Sequence 2, Appli	460	6	4.4	431	15	US-10-369-493-13170	Sequence 13170, A
388	6	4.4	346	14	US-10-336-587-2	Sequence 2, Appli	461	6	4.4	433	15	US-10-369-493-17028	Sequence 17028, A
389	6	4.4	347	16	US-10-437-963-151641	Sequence 151641, A	462	6	4.4	433	15	US-10-282-122A-5814	Sequence 5814, A
390	6	4.4	348	16	US-10-425-115-283510	Sequence 283510, A	463	6	4.4	434	15	US-10-282-122A-55156	Sequence 55156, A
391	6	4.4	349	17	US-10-857-244-1	Sequence 1, Appli	464	6	4.4	434	15	US-10-282-122A-67746	Sequence 67746, A
392	6	4.4	351	15	US-10-282-122A-46888	Sequence 46888, A	465	6	4.4	438	15	US-10-425-114-69760	Sequence 69760, A
393	6	4.4	356	9	US-09-738-626-4781	Sequence 4781, Ap	466	6	4.4	440	15	US-10-116-275-335	Sequence 335, App
394	6	4.4	360	15	US-10-424-599-277493	Sequence 277493, A	467	6	4.4	441	15	US-10-116-275-132	Sequence 132, App
395	6	4.4	362	9	US-09-767-870-10	Sequence 10, Appl	468	6	4.4	444	15	US-10-425-114-42253	Sequence 42253, A
396	6	4.4	362	14	US-10-242-568-10	Sequence 10, Appl	469	6	4.4	445	15	US-10-425-114-48747	Sequence 48747, A
397	6	4.4	364	15	US-10-425-114-71421	Sequence 71421, A	470	6	4.4	445	15	US-10-425-114-50214	Sequence 50214, A
398	6	4.4	365	15	US-10-369-493-13933	Sequence 13933, A	471	6	4.4	445	15	US-10-335-977-6503	Sequence 6503, Ap
399	6	4.4	365	16	US-10-767-701-44242	Sequence 44242, A	472	6	4.4	447	15	US-10-424-599-208750	Sequence 208750, A
400	6	4.4	366	15	US-10-369-493-13763	Sequence 13763, A	473	6	4.4	451	15	US-10-369-493-9788	Sequence 9788, Ap
401	6	4.4	368	15	US-10-389-566-382	Sequence 382, App	474	6	4.4	451	16	US-10-425-115-199924	Sequence 199924, A
402	6	4.4	369	16	US-10-425-115-253705	Sequence 253705, A	475	6	4.4	452	14	US-10-238-075-504	Sequence 504, App
403	6	4.4	371	15	US-10-424-599-221879	Sequence 221879, A	476	6	4.4	453	15	US-10-369-493-4172	Sequence 4172, Ap
404	6	4.4	371	16	US-10-437-963-122405	Sequence 122405, A	477	6	4.4	458	16	US-10-425-115-187669	Sequence 187669, A
405	6	4.4	372	15	US-10-369-493-23206	Sequence 23206, A	478	6	4.4	461	14	US-10-187-267A-59	Sequence 59, Appl
406	6	4.4	374	15	US-10-425-114-44541	Sequence 44541, A	479	6	4.4	461	15	US-10-369-493-23446	Sequence 23446, A
407	6	4.4	377	15	US-10-425-114-44189	Sequence 44189, A	480	6	4.4	462	15	US-10-282-122A-61794	Sequence 61794, A
408	6	4.4	382	15	US-10-425-114-43420	Sequence 43420, A	481	6	4.4	465	13	US-10-087-192-348	Sequence 348, App
409	6	4.4	383	17	US-10-732-923-18897	Sequence 18897, A	482	6	4.4	470	13	US-10-087-192-345	Sequence 345, App
410	6	4.4	384	9	US-09-853-918-20	Sequence 20, Appl	483	6	4.4	470	16	US-10-004-378A-103	Sequence 103, App
411	6	4.4	384	9	US-09-853-918-21	Sequence 21, Appl	484	6	4.4	470	16	US-10-437-963-172330	Sequence 172330, A
412	6	4.4	384	9	US-09-853-918-22	Sequence 22, Appl	485	6	4.4	473	17	US-10-732-923-9640	Sequence 9640, Ap
413	6	4.4	384	9	US-09-853-918-23	Sequence 23, Appl	486	6	4.4	474	15	US-10-425-114-62699	Sequence 62699, A
414	6	4.4	384	9	US-09-853-918-24	Sequence 24, Appl	487	6	4.4	474	15	US-10-425-114-63550	Sequence 63550, A
415	6	4.4	384	9	US-09-853-918-25	Sequence 25, Appl	488	6	4.4	475	15	US-10-108-260A-3563	Sequence 3563, Ap
416	6	4.4	384	9	US-09-853-918-26	Sequence 26, Appl	489	6	4.4	476	15	US-10-282-122A-73039	Sequence 73039, A
417	6	4.4	384	9	US-09-853-918-27	Sequence 27, Appl	490	6	4.4	477	15	US-10-282-122A-64300	Sequence 64300, A
418	6	4.4	384	9	US-09-853-918-28	Sequence 28, Appl	491	6	4.4	481	9	US-09-738-626-6986	Sequence 6986, Ap
419	6	4.4	384	9	US-09-853-918-29	Sequence 29, Appl	492	6	4.4	481	16	US-10-432-934-29	Sequence 29, Appl
420	6	4.4	384	16	US-10-437-963-123212	Sequence 123212, A	493	6	4.4	481	16	US-10-739-930-6313	Sequence 6313, Ap
421	6	4.4	384	16	US-10-437-963-203365	Sequence 203365, A	494	6	4.4	482	14	US-10-156-761-12787	Sequence 12787, A
422	6	4.4	385	9	US-09-853-918-31	Sequence 31, Appl	495	6	4.4	487	14	US-10-156-761-11764	Sequence 11764, A
423	6	4.4	385	9	US-09-853-918-32	Sequence 32, Appl	496	6	4.4	487	15	US-10-369-493-6111	Sequence 6111, Ap
424	6	4.4	385	9	US-09-853-918-33	Sequence 33, Appl	497	6	4.4	487	15	US-10-282-122A-68809	Sequence 68809, A
425	6	4.4	385	9	US-09-853-918-34	Sequence 34, Appl	498	6	4.4	490	16	US-10-755-889-44	Sequence 44, Appl
426	6	4.4	385	9	US-09-853-918-35	Sequence 35, Appl	499	6	4.4	491	9	US-09-741-669-455	Sequence 455, App
427	6	4.4	385	9	US-09-853-918-36	Sequence 36, Appl	500	6	4.4	491	9	US-09-815-242-10032	Sequence 10032, A
428	6	4.4	385	9	US-09-853-918-37	Sequence 37, Appl	501	6	4.4	491	9	US-09-815-242-14079	Sequence 14079, A
429	6	4.4	385	9	US-09-853-918-38	Sequence 38, Appl	502	6	4.4	491	15	US-10-282-122A-55678	Sequence 55678, A
430	6	4.4	385	9	US-09-853-918-39	Sequence 39, Appl	503	6	4.4	491	15	US-10-282-122A-56416	Sequence 56416, A
431	6	4.4	388	15	US-10-369-493-6340	Sequence 6340, Ap	504	6	4.4	491	15	US-10-282-122A-59579	Sequence 59579, A
432	6	4.4	390	15	US-10-972-546-8	Sequence 8, Appli	505	6	4.4	491	15	US-10-282-122A-75190	Sequence 75190, A
433	6	4.4	390	15	US-10-369-493-5440	Sequence 5440, Ap	506	6	4.4	491	15	US-10-282-122A-76022	Sequence 76022, A
434	6	4.4	390	17	US-10-369-493-19231	Sequence 19231, A	507	6	4.4	491	15	US-10-282-122A-77927	Sequence 77927, A
435	6	4.4	392	16	US-10-437-963-125207	Sequence 125207, A	508	6	4.4	492	9	US-09-895-072-19	Sequence 19, Appl
436	6	4.4	392	15	US-10-369-493-17281	Sequence 17281, A	509	6	4.4	492	9	US-09-986-552-19	Sequence 19, Appl
437	6	4.4	395	15	US-10-369-493-13723	Sequence 13723, A	510	6	4.4	492	14	US-10-023-888-20	Sequence 20, Appl
438	6	4.4	395	15	US-10-424-599-261235	Sequence 261235, A	511	6	4.4	492	14	US-10-023-889-20	Sequence 20, Appl
439	6	4.4	398	16	US-10-424-599-261235	Sequence 8464, Ap	512	6	4.4	492	14	US-10-023-890-20	Sequence 20, Appl
440	6	4.4	399	15	US-10-369-493-8464	Sequence 46819, A	513	6	4.4	492	14	US-10-024-197-20	Sequence 20, Appl
441	6	4.4	401	14	US-10-282-122A-46839	Sequence 97, Appl	514	6	4.4	492	14	US-10-023-894-20	Sequence 20, Appl
442	6	4.4	401	14	US-10-050-704-97	Sequence 97, Appl	515	6	4.4	492	17	US-10-306-686-19	Sequence 19, Appl
443	6	4.4	401	16	US-10-798-512-97	Sequence 17, Appl	516	6	4.4	492	17	US-10-901-216-20	Sequence 20, Appl
444	6	4.4	401	17	US-10-477-714-17	Sequence 17, Appl	517	6	4.4	492	17	US-10-494-672-72	Sequence 72, Appl
445	6	4.4	403	15	US-10-369-493-19185	Sequence 19185, A	518	6	4.4	492	17	US-10-494-672-72	Sequence 72, Appl
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525	6	4.4	512	15	US-10-369-493-14356	Sequence 14356, A	598	6	4.4	565	15	US-10-418-036-10	Sequence 10, Appl
526	6	4.4	512	15	US-10-369-493-14613	Sequence 14613, A	599	6	4.4	565	15	US-10-618-839-10	Sequence 10, Appl
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529	6	4.4	514	9	US-09-853-918-49	Sequence 49, Appl	602	6	4.4	565	20	US-11-069-161-10	Sequence 10, Appl
530	6	4.4	514	9	US-09-853-918-63	Sequence 63, Appl	603	6	4.4	568	15	US-10-369-493-10876	Sequence 10876, A
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535	6	4.4	514	10	US-09-846-637A-10	Sequence 10, Appl	608	6	4.4	573	17	US-10-732-923-10708	Sequence 10708, A
536	6	4.4	514	10	US-09-846-637A-12	Sequence 12, Appl	609	6	4.4	577	15	US-10-382-122A-50518	Sequence 50518, A
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544	6	4.4	515	9	US-09-985-552-6	Sequence 6, Appl	617	6	4.4	601	9	US-09-887-586A-42	Sequence 42, Appl
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573	6	4.4	540	16	US-10-719-993-615	Sequence 615, App	645	6	4.4	650	16	US-10-425-115-310869	Sequence 310869, A
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586	6	4.4	558	14	US-10-156-761-13528	Sequence 13528, A	658	6	4.4	676	16	US-10-437-963-114875	Sequence 114875, A
587	6	4.4	558	15	US-10-108-260A-4274	Sequence 4274, Ap	659	6	4.4	695	15	US-10-108-260A-3799	Sequence 3799, Ap
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591	6	4.4	560	15	US-10-369-493-14621	Sequence 14621, A	663	6	4.4	699	15	US-10-369-493-1430	Sequence 1430, Ap
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593	6	4.4	561	18	US-10-431-241-16	Sequence 16, Appl	665	6	4.4	699	16	US-10-451-467A-40	Sequence 40, Appl
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671	6	4.4	714	15	US-10-425-114-62753	Sequence 62753, A	744	6	4.4	888	14	US-10-123-262-544	Sequence 544, App
672	6	4.4	722	9	US-09-894-998-15	Sequence 15, Appl	745	6	4.4	888	14	US-10-142-423-544	Sequence 544, App
673	6	4.4	722	14	US-10-121-988-15	Sequence 15, Appl	746	6	4.4	888	14	US-10-121-050-544	Sequence 544, App
674	6	4.4	722	14	US-10-121-988-159	Sequence 159, App	747	6	4.4	888	14	US-10-141-755-544	Sequence 544, App
675	6	4.4	722	14	US-10-200-562-15	Sequence 15, Appl	748	6	4.4	888	14	US-10-143-032-544	Sequence 544, App
676	6	4.4	722	14	US-10-200-562-159	Sequence 159, App	749	6	4.4	888	14	US-10-123-108-544	Sequence 544, App
677	6	4.4	722	14	US-10-237-551-15	Sequence 15, Appl	750	6	4.4	888	14	US-10-123-236-544	Sequence 544, App
678	6	4.4	722	14	US-10-237-551-159	Sequence 159, App	751	6	4.4	888	14	US-10-123-261-544	Sequence 544, App
679	6	4.4	722	14	US-10-237-551-235	Sequence 235, App	752	6	4.4	888	14	US-10-140-921-544	Sequence 544, App
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682	6	4.4	722	18	US-10-945-050-159	Sequence 159, App	755	6	4.4	888	14	US-10-123-292-544	Sequence 544, App
683	6	4.4	722	18	US-10-945-050-235	Sequence 235, App	756	6	4.4	888	14	US-10-123-903-544	Sequence 544, App
684	6	4.4	738	15	US-10-369-493-2442	Sequence 2442, Ap	757	6	4.4	888	14	US-10-124-819-544	Sequence 544, App
685	6	4.4	738	17	US-10-732-923-22103	Sequence 22103, A	758	6	4.4	888	14	US-10-124-822-544	Sequence 544, App
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687	6	4.4	739	15	US-10-369-493-2516	Sequence 2516, Ap	760	6	4.4	888	14	US-10-160-498-544	Sequence 544, App
688	6	4.4	739	16	US-10-408-765A-774	Sequence 774, App	761	6	4.4	888	14	US-10-124-824-544	Sequence 544, App
689	6	4.4	739	16	US-10-408-765A-775	Sequence 775, App	762	6	4.4	888	14	US-10-127-825A-544	Sequence 544, App
690	6	4.4	752	9	US-09-815-242-10281	Sequence 10281, A	763	6	4.4	888	14	US-10-127-829A-544	Sequence 544, App
691	6	4.4	752	15	US-10-282-122A-43043	Sequence 43043, A	764	6	4.4	888	14	US-10-127-835A-544	Sequence 544, App
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693	6	4.4	759	15	US-10-424-599-186567	Sequence 186567, A	766	6	4.4	888	14	US-10-127-901A-544	Sequence 544, App
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695	6	4.4	767	17	US-10-732-923-12319	Sequence 12319, A	768	6	4.4	888	14	US-10-131-813A-544	Sequence 544, App
696	6	4.4	769	17	US-10-732-923-12321	Sequence 12321, A	769	6	4.4	888	14	US-10-131-818A-544	Sequence 544, App
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698	6	4.4	773	16	US-10-437-963-141759	Sequence 141759, A	771	6	4.4	888	14	US-10-131-824A-544	Sequence 544, App
699	6	4.4	776	17	US-10-732-923-22102	Sequence 22102, A	772	6	4.4	888	14	US-10-131-830A-544	Sequence 544, App
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701	6	4.4	785	14	US-10-043-487-260	Sequence 260, App	774	6	4.4	888	14	US-10-137-872A-544	Sequence 544, App
702	6	4.4	785	15	US-10-126-103-152	Sequence 152, App	775	6	4.4	888	14	US-10-147-500-544	Sequence 544, App
703	6	4.4	785	15	US-10-431-096-152	Sequence 152, App	776	6	4.4	888	14	US-10-147-502-544	Sequence 544, App
704	6	4.4	785	16	US-10-408-765A-1047	Sequence 1047, Ap	777	6	4.4	888	14	US-10-147-515-544	Sequence 544, App
705	6	4.4	785	17	US-10-732-923-22101	Sequence 22101, A	778	6	4.4	888	14	US-10-147-517-544	Sequence 544, App
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707	6	4.4	791	14	US-10-156-761-12134	Sequence 12134, A	780	6	4.4	888	14	US-10-147-527-544	Sequence 544, App
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712	6	4.4	808	16	US-10-437-963-127182	Sequence 127182, A	785	6	4.4	888	14	US-10-123-902-544	Sequence 544, App
713	6	4.4	815	15	US-10-108-260A-4238	Sequence 4238, Ap	786	6	4.4	888	14	US-10-123-908-544	Sequence 544, App
714	6	4.4	822	15	US-10-320-797-3301	Sequence 3301, Ap	787	6	4.4	888	14	US-10-123-909-544	Sequence 544, App
715	6	4.4	831	16	US-10-437-963-194578	Sequence 194578, A	788	6	4.4	888	14	US-10-123-910-544	Sequence 544, App
716	6	4.4	832	15	US-10-369-493-1540	Sequence 1540, Ap	789	6	4.4	888	14	US-10-124-813-544	Sequence 544, App
717	6	4.4	832	15	US-10-149-310-242	Sequence 242, App	790	6	4.4	888	14	US-10-124-817-544	Sequence 544, App
718	6	4.4	837	15	US-10-369-493-18586	Sequence 18586, A	791	6	4.4	888	14	US-10-125-922-544	Sequence 544, App
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720	6	4.4	881	16	US-10-425-115-293707	Sequence 293707, A	793	6	4.4	888	14	US-10-140-860-544	Sequence 544, App
721	6	4.4	885	16	US-10-437-963-139936	Sequence 139936, A	79336	6	4.4	888	14	US-10-142-417-544	Sequence 544, App
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723	6	4.4	888	13	US-10-036-342-35	Sequence 35, Appl	796	6	4.4	888	14	US-10-157-782-544	Sequence 544, App
724	6	4.4	888	13	US-10-036-041-35	Sequence 35, Appl	797	6	4.4	888	14	US-10-152-395-544	Sequence 544, App
725	6	4.4	888	14	US-10-028-072-544	Sequence 544, App	798	6	4.4	888	14	US-10-125-926A-544	Sequence 544, App
726	6	4.4	888	14	US-10-035-855-35	Sequence 35, Appl	799	6	4.4	888	14	US-10-125-930A-544	Sequence 544, App
727	6	4.4	888	14	US-10-140-808-544	Sequence 544, App	800	6	4.4	888	14	US-10-127-831A-544	Sequence 544, App
728	6	4.4	888	14	US-10-121-049-544	Sequence 544, App	801	6	4.4	888	14	US-10-127-837A-544	Sequence 544, App
729	6	4.4	888	14	US-10-123-904-544	Sequence 544, App	802	6	4.4	888	14	US-10-127-838B-544	Sequence 544, App
730	6	4.4	888	14	US-10-140-470-544	Sequence 544, App	803	6	4.4	888	14	US-10-127-842A-544	Sequence 544, App
731	6	4.4	888	14	US-10-175-746-544	Sequence 544, App	804	6	4.4	888	14	US-10-127-843A-544	Sequence 544, App
732	6	4.4	888	14	US-10-176-918-544	Sequence 544, App	805	6	4.4	888	14	US-10-127-845A-544	Sequence 544, App
733	6	4.4	888	14	US-10-176-921-544	Sequence 544, App	806	6	4.4	888	14	US-10-127-846A-544	Sequence 544, App
734	6	4.4	888	14	US-10-036-214-35	Sequence 35, Appl	807	6	4.4	888	14	US-10-127-849A-544	Sequence 544, App
735	6	4.4	888	14	US-10-137-865-544	Sequence 544, App	808	6	4.4	888	14	US-10-127-849A-544	Sequence 544, App
736	6	4.4	888	14	US-10-140-474-544	Sequence 544, App	809	6	4.4	888	14	US-10-127-850A-544	Sequence 544, App
737	6	4.4	888	14	US-10-035-719-35	Sequence 35, Appl	810	6	4.4	888	14	US-10-127-851A-544	Sequence 544, App
738	6	4.4	888	14	US-10-142-431-544	Sequence 544, App	811	6	4.4	888	14	US-10-128-684A-544	Sequence 544, App
739	6	4.4	888	14	US-10-143-114-544	Sequence 544, App	812	6	4.4	888	14	US-10-128-686A-544	Sequence 544, App
740	6	4.4	888	14	US-10-036-160-35	Sequence 35, Appl	813	6	4.4	888	14	US-10-128-690A-544	Sequence 544, App
741	6	4.4	888	14	US-10-142-419-544	Sequence 544, App	814	6	4.4	888	14	US-10-128-691A-544	Sequence 544, App


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961 6 4.4 888 14 US-10-145-747-544 Sequence 544, App
962 6 4.4 888 14 US-10-145-752-544 Sequence 544, App
963 6 4.4 888 14 US-10-145-754-544 Sequence 544, App
964 6 4.4 888 14 US-10-145-755-544 Sequence 544, App
965 6 4.4 888 14 US-10-145-818-544 Sequence 544, App
966 6 4.4 888 14 US-10-145-820-544 Sequence 544, App
967 6 4.4 888 14 US-10-145-872-544 Sequence 544, App
968 6 4.4 888 14 US-10-145-873-544 Sequence 544, App
969 6 4.4 888 14 US-10-147-481-544 Sequence 544, App
970 6 4.4 888 14 US-10-147-482-544 Sequence 544, App
971 6 4.4 888 14 US-10-147-503-544 Sequence 544, App
972 6 4.4 888 14 US-10-147-522-544 Sequence 544, App
973 6 4.4 888 14 US-10-152-401-544 Sequence 544, App
974 6 4.4 888 14 US-10-157-783-544 Sequence 544, App
975 6 4.4 888 14 US-10-158-792-544 Sequence 544, App
976 6 4.4 888 14 US-10-158-792-544 Sequence 544, App
977 6 4.4 888 14 US-10-158-792-544 Sequence 544, App
978 6 4.4 888 14 US-10-143-035-544 Sequence 544, App
979 6 4.4 888 14 US-10-145-751-544 Sequence 544, App
980 6 4.4 888 14 US-10-145-822-544 Sequence 544, App
981 6 4.4 888 14 US-10-145-824-544 Sequence 544, App
982 6 4.4 888 14 US-10-145-827-544 Sequence 544, App
983 6 4.4 888 14 US-10-145-869-544 Sequence 544, App
984 6 4.4 888 14 US-10-145-875-544 Sequence 544, App
985 6 4.4 888 14 US-10-145-877-544 Sequence 544, App
986 6 4.4 888 14 US-10-145-958-544 Sequence 544, App
987 6 4.4 888 14 US-10-146-787-544 Sequence 544, App
988 6 4.4 888 14 US-10-146-790-544 Sequence 544, App
989 6 4.4 888 14 US-10-146-793-544 Sequence 544, App
990 6 4.4 888 14 US-10-147-480-544 Sequence 544, App
991 6 4.4 888 14 US-10-147-485-544 Sequence 544, App
992 6 4.4 888 14 US-10-147-486-544 Sequence 544, App
993 6 4.4 888 14 US-10-147-487-544 Sequence 544, App
994 6 4.4 888 14 US-10-147-490-544 Sequence 544, App
995 6 4.4 888 14 US-10-147-494-544 Sequence 544, App
996 6 4.4 888 14 US-10-147-498-544 Sequence 544, App
997 6 4.4 888 14 US-10-147-514-544 Sequence 544, App
998 6 4.4 888 14 US-10-147-524-544 Sequence 544, App
999 6 4.4 888 14 US-10-152-379-544 Sequence 544, App
1000 6 4.4 888 17 US-10-158-788-544 Sequence 544, App

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ALIGNMENTS

```

RESULT 1
US-10-473-127-424
; Sequence 424, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 424
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-473-127-424
Query Match 100.0%; Score 135; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPYDGNVGRGYLSVFL 60
Db 271 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPYDGNVGRGYLSVFL 330
Qy 61 LSAGLPETSKYEVREVMVHQSNDPTKNIIRFASDFEVCWCYNRFFRLDLLANEGYL 120
Db 331 LSAGLPETSKYEVREVMVHQSNDPTKNIIRFASDFEVCWCYNRFFRLDLLANEGYL 390
Qy 121 NPQNDTVILRFQVRS 135
Db 391 NPQNDTVILRFQVRS 405

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RESULT 2

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US-10-473-127-429
; Sequence 429, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 429
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-429
Query Match 100.0%; Score 135; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPYDGNVGRGYLSVFL 60
Db 271 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPYDGNVGRGYLSVFL 330
Qy 61 LSAGLPETSKYEVREVMVHQSNDPTKNIIRFASDFEVCWCYNRFFRLDLLANEGYL 120
Db 331 LSAGLPETSKYEVREVMVHQSNDPTKNIIRFASDFEVCWCYNRFFRLDLLANEGYL 390
Qy 121 NPQNDTVILRFQVRS 135
Db 391 NPQNDTVILRFQVRS 405

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RESULT 3

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US-10-473-127-431
; Sequence 431, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING

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; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 431
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-431

Query Match      100.0%; Score 135; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLKVKYDPDNGVVRGYLSVFE 60
Db      271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLKVKYDPDNGVVRGYLSVFE 330

Qy      61 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWCYNRFRLLDLLANEGYL 120
Db      331 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWCYNRFRLLDLLANEGYL 390

Qy      121 NPQNDTVILRFQVRS 135
Db      391 NPQNDTVILRFQVRS 405

RESULT 4
US-10-473-127-423
; Sequence 423, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 423
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-423

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLKVKYDPDNGVVRGYLSVFE 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLKVKYDPDNGVVRGYLSVFE 345

Qy      61 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWCYNRFRLLDLLANEGYL 120
Db      346 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWCYNRFRLLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 5
US-10-473-127-425
; Sequence 425, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-425

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLKVKYDPDNGVVRGYLSVFE 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLKVKYDPDNGVVRGYLSVFE 345

Qy      61 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWCYNRFRLLDLLANEGYL 120
Db      346 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWCYNRFRLLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 6
US-10-473-127-426
; Sequence 426, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
```

```
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 426
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-426

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 345

Qy      61  LSAGLPETSKYEVYRVMVHQSCNDPTKNIITREFASDFEVCWCWYRFFRLDLLANEGYL 120
Db      346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIITREFASDFEVCWCWYRFFRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 7
US-10-473-127-427
; Sequence 427, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-427

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 345

Qy      61  LSAGLPETSKYEVYRVMVHQSCNDPTKNIITREFASDFEVCWCWYRFFRLDLLANEGYL 120
Db      346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIITREFASDFEVCWCWYRFFRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420
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```
Qy      61  LSAGLPETSKYEVYRVMVHQSCNDPTKNIITREFASDFEVCWCWYRFFRLDLLANEGYL 120
Db      346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIITREFASDFEVCWCWYRFFRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 8
US-10-473-127-432
; Sequence 432, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 432
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-432

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 345

Qy      61  LSAGLPETSKYEVYRVMVHQSCNDPTKNIITREFASDFEVCWCWYRFFRLDLLANEGYL 120
Db      346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIITREFASDFEVCWCWYRFFRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 9
US-10-473-127-430
; Sequence 430, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
```

;; PRIOR FILING DATE: 2001-10-01
;; PRIOR APPLICATION NUMBER: 60/336,780
;; PRIOR FILING DATE: 2001-12-04
;; PRIOR APPLICATION NUMBER: 60/358,985
;; PRIOR FILING DATE: 2002-02-20
;; NUMBER OF SEQ ID NOS: 2041
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 430
;; LENGTH: 1016
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-473-127-430

Query Match 100.0%; Score 135; DB 16; Length 1016;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKYPPDNGVVRGYLSVFL 60
DB 323 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKYPPDNGVVRGYLSVFL 382
QY 61 LSAGLPETSKYRYRVMVHQSCNDPTKNIIRFASDFEVEGCGVNRFRRLDLLANEGYL 120
DB 383 LSAGLPETSKYRYRVMVHQSCNDPTKNIIRFASDFEVEGCGVNRFRRLDLLANEGYL 442
QY 121 NPQDVTILRFQVRS 135
DB 443 NPQDVTILRFQVRS 457

RESULT 10
US-10-473-127-428
;; Sequence 428, Application US/10473127
;; Publication No. US20040236091A1
;; GENERAL INFORMATION:
;; APPLICANT: Zycos Inc.
;; TITLE OF INVENTION: TRANSLATIONAL PROFILING
;; FILE REFERENCE: 08191-026W01
;; CURRENT APPLICATION NUMBER: US/10/473,127
;; CURRENT FILING DATE: 2003-09-26
;; PRIOR APPLICATION NUMBER: 60/279,495
;; PRIOR FILING DATE: 2001-03-28
;; PRIOR APPLICATION NUMBER: 60/292,544
;; PRIOR FILING DATE: 2001-05-21
;; PRIOR APPLICATION NUMBER: 60/310,801
;; PRIOR FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: 60/326,370
;; PRIOR FILING DATE: 2001-10-01
;; PRIOR APPLICATION NUMBER: 60/336,780
;; PRIOR FILING DATE: 2001-12-04
;; PRIOR APPLICATION NUMBER: 60/358,985
;; PRIOR FILING DATE: 2002-02-20
;; NUMBER OF SEQ ID NOS: 2041
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 428
;; LENGTH: 964
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-473-127-428

Query Match 67.4%; Score 91; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKYPPDNGVVRGYLSVFL 60
DB 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKYPPDNGVVRGYLSVFL 330
QY 61 LSAGLPETSKYRYRVMVHQSCNDPTKNIIR 91
DB 331 LSAGLPETSKYRYRVMVHQSCNDPTKNIIR 361

RESULT 11
US-09-992-238-33
;; Sequence 33, Application US/09992238
;; Publication No. US2003005444A1
;; GENERAL INFORMATION:
;; APPLICANT: BATTAGLINO, PETER
;; APPLICANT: FEDER, JOHN N
;; APPLICANT: MINTIER, GABE
;; APPLICANT: NELSON, THOMAS C
;; APPLICANT: RAMANATHAN, CHANDRA S
;; APPLICANT: WESTPHAL, RYAN
;; APPLICANT: CACACE, ANGELA
;; APPLICANT: BARBER, LAUREN
;; APPLICANT: HAWKEN, DONALD R
;; APPLICANT: KORNACKER, MICHAEL G
;; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV8,
;; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN
;; FILE REFERENCE: D0047NP
;; CURRENT APPLICATION NUMBER: US/09/992,238
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/317166
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: 60/308285
;; PRIOR FILING DATE: 2001-07-27
;; PRIOR APPLICATION NUMBER: 60/268581
;; PRIOR FILING DATE: 2001-02-14
;; PRIOR APPLICATION NUMBER: 60/248285
;; PRIOR FILING DATE: 2000-11-14
;; NUMBER OF SEQ ID NOS: 102
;; SOFTWARE: Patent in Ver. 2.1
;; SEQ ID NO 33
;; LENGTH: 55
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthesized
;; OTHER INFORMATION: peptide
US-09-992-238-33

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Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPSYDSATF 11
DB 46 VPSYDSATF 54

RESULT 12
US-10-712-615-33
;; Sequence 33, Application US/10712615
;; Publication No. US20040214317A1
;; GENERAL INFORMATION:
;; APPLICANT: Bristol-Myers Squibb Company
;; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV8, EXPRESSED
;; TITLE OF INVENTION: HIGHLY IN BRAIN
;; FILE REFERENCE: D0047A-CIP
;; CURRENT APPLICATION NUMBER: US/10/712,615
;; CURRENT FILING DATE: 2003-11-13
;; PRIOR APPLICATION NUMBER: U.S. 09/992,238
;; PRIOR FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: U.S. 60/248,285
;; PRIOR FILING DATE: 2000-11-14
;; PRIOR APPLICATION NUMBER: U.S. 60/268,581
;; PRIOR FILING DATE: 2001-02-14
;; PRIOR APPLICATION NUMBER: U.S. 60/308,285
;; PRIOR FILING DATE: 2001-07-27
;; PRIOR APPLICATION NUMBER: U.S. 60/317,166
;; PRIOR FILING DATE: 2001-09-04
;; NUMBER OF SEQ ID NOS: 134
;; SOFTWARE: Patent in version 3.2
;; SEQ ID NO 33
;; LENGTH: 55

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-712-615-33

Query Match          6.7%; Score 9; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      46 VPSYDSATF 54

RESULT 13
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; Sequence 115, Application US/09828644
; Patent No. US20020015998A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US20020015998A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00196US1
; CURRENT APPLICATION NUMBER: US/09/828,644
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,150
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,099
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,151
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,148
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,093
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,098
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/230,149
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-644-115

Query Match          6.7%; Score 9; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      172 VPSYDSATF 180

RESULT 14
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; Sequence 2, Application US/09841741
; Publication No. US20030170779A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US20030170779A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00204.REGUS
; CURRENT APPLICATION NUMBER: US/09/841,741
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: USSN 60/199,558
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-841-741-2

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Qy      3 VPSYDSATF 11
Db      389 VPSYDSATF 397

RESULT 15
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; Sequence 5, Application US/10345332
; Publication No. US20030129705A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00754CON
; CURRENT APPLICATION NUMBER: US/10/345,332
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/769,741
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/205,166
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/638,018
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-345-332-5

Query Match          6.7%; Score 9; DB 14; Length 398;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 VPSYDSATF 11
Db      389 VPSYDSATF 397

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OM protein - protein search, using sw model

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Title: US-09-706-325-25

Perfect score: 135

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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- 2: geneseqp1990s:*
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- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	135	100.0	964	6	Abu03765 Human exp
6	135	100.0	964	6	Abu03758 Human exp
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9	135	100.0	979	6	Abu03766 Human exp
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25	9	6.7	485	7	Adc86473 Human GFC

26	9	6.7	485	7	ADD18025	Human G-p
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28	9	6.7	508	4	AAB61982	Human G-p
29	9	6.7	508	4	AAU25605	Human G p
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45	9	6.7	508	6	ABP81704	Human G p
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52	9	6.7	508	8	ADO29034	Human nov
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57	8	5.9	314	6	ABU19048	Protein e
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61	7	5.2	198	6	ABU25828	Protein e
62	7	5.2	243	4	AAW41864	Human pol
63	7	5.2	244	4	ABG25183	Novel hum
64	7	5.2	285	4	ABG96337	Putative
65	7	5.2	357	4	AAG89758	C Glutami
66	7	5.2	378	8	ADN25671	Bacterial
67	7	5.2	389	4	AAU50335	Propionib
68	7	5.2	389	6	ABW46854	Propionib
69	7	5.2	411	2	AAW97718	Staphyloc
70	7	5.2	419	4	ABG23515	Novel hum
71	7	5.2	441	4	ABB63022	Drosophil
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73	7	5.2	518	4	ABG04092	Novel hum
74	7	5.2	548	6	ABM72915	Staphyloc
75	7	5.2	548	7	ABO72047	Pseudomon
76	7	5.2	561	5	ABG97480	Human NOV
77	7	5.2	651	3	AAAB10936	Human RNA
78	7	5.2	651	5	ABW78308	Amino aci
79	7	5.2	806	6	ABM69133	Phototrab
80	6	4.4	14	5	ABG92758	A. nidula
81	6	4.4	21	7	ABO23430	Amino aci
82	6	4.4	21	8	ADR20818	Human sec
83	6	4.4	32	4	AAW88014	Human imm
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85	6	4.4	35	4	ABH37739	Peptide #
86	6	4.4	41	2	AAW80399	A secree
87	6	4.4	50	4	AAU13844	Human pol
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91	6	4.4	51	6	ABM52292	Propionib
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96	6	4.4	59	4	AAO2813	Human pol
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98	6	4.4	63	3	AAAB07696	A human 1

99	6	4.4	63	3	AB07605	Ab07605 A human i	172	6	4.4	141	3	AAG03814	As03814 Human sec
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101	6	4.4	63	8	ADRI3820	Adri3820 Human int	174	6	4.4	141	7	ADMO4482	Adm04482 Human pro
102	6	4.4	67	4	AU44848	Au44848 Propionib	175	6	4.4	141	8	ADO20222	Ado20222 Human pro
103	6	4.4	67	6	ABM41367	Abm41367 Propionib	176	6	4.4	141	8	ADR20816	Adr20816 Human sec
104	6	4.4	68	2	AY12781	Aay12781 Human 5'	177	6	4.4	141	8	ABM81507	Abm81507 Tumour-as
105	6	4.4	69	6	ADA33640	Ada33640 Acinetoba	178	6	4.4	141	8	ADP55186	Adp55186 Human PRO
106	6	4.4	73	4	AAO07952	Aao07952 Human pol	179	6	4.4	141	8	ADP24812	Adp24812 PRO polyp
107	6	4.4	74	4	AAO05691	Aao05691 Human pol	180	6	4.4	142	2	AY29012	Aay29012 T. gondii
108	6	4.4	77	3	AG02196	Ag02196 Human sec	181	6	4.4	142	4	AAU25483	Aau25483 T. gondii
109	6	4.4	79	7	ABO65292	Ab065292 Klebsiell	182	6	4.4	142	7	ADG17074	Adg17074 T. gondii
110	6	4.4	80	2	AAV36439	Aav36439 Fragment	183	6	4.4	143	8	ADR09379	Adr09379 Human pro
111	6	4.4	80	3	AAV36439	Aav36439 Fragment	184	6	4.4	143	8	ABR89243	Ab889243 Human pol
112	6	4.4	80	4	ADM19701	Adm19701 Protein e	185	6	4.4	144	5	ABR89243	Ab889243 Human pol
113	6	4.4	80	4	ADM19701	Adm19701 Protein e	186	6	4.4	144	5	ABR89243	Ab889243 Human pol
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115	6	4.4	81	4	AAU20343	Aau20343 Human sec	188	6	4.4	145	6	ABM40301	Abm40301 Propionib
116	6	4.4	81	8	AAO12540	Aao12540 Human pol	189	6	4.4	147	3	AAU41086	Aau41086 Human ORF
117	6	4.4	88	3	ABM41970	Abm41970 Human ORF	190	6	4.4	147	4	AAU55797	Aau55797 Propionib
118	6	4.4	90	4	AAU50831	Aau50831 Propionib	191	6	4.4	147	5	ABP34694	Abp34694 Human ORF
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120	6	4.4	92	7	ADF60180	Adf60180 Human con	193	6	4.4	150	4	AAU523508	Aau523508 Rat EST e
121	6	4.4	94	6	AAU50268	Aau50268 Propionib	194	6	4.4	150	6	ABO00769	Ab000769 Polypepti
122	6	4.4	94	6	ABM46787	Abm46787 Propionib	195	6	4.4	150	8	ADL30880	Adl30880 Human pro
123	6	4.4	96	3	AG54437	Ag54437 Zee mays	196	6	4.4	151	4	AAU92654	Aau92654 Human dig
124	6	4.4	96	4	AAO02838	Aao02838 Human pol	197	6	4.4	151	4	AAU22648	Aau22648 Novel hum
125	6	4.4	97	5	ABP31142	Abp31142 Human per	198	6	4.4	151	7	ADB32488	Adb32488 Human nov
126	6	4.4	98	3	AG41173	Ag41173 Zee mays	199	6	4.4	153	5	ABU51799	Abu51799 Helicobac
127	6	4.4	98	4	AAU59025	Aau59025 Propionib	200	6	4.4	154	4	AAU25921	Aau25921 Human pro
128	6	4.4	98	6	ABM55544	Abm55544 Propionib	201	6	4.4	157	4	AAU25818	Aau25818 Human pro
129	6	4.4	99	4	AAU45195	Aau45195 Propionib	202	6	4.4	157	5	ABP29925	Abp29925 Streptoco
130	6	4.4	99	4	AAU20902	Aau20902 Human nov	203	6	4.4	157	5	ABP30763	Abp30763 Streptoco
131	6	4.4	99	6	ABM41714	Abm41714 Propionib	204	6	4.4	158	4	AAU19193	Aau19193 Human G p
132	6	4.4	99	6	ADA48310	Ada48310 Rice prot	205	6	4.4	158	4	AAU48532	Aau48532 Propionib
133	6	4.4	100	3	AAU00687	Aau00687 Human sec	206	6	4.4	158	6	ABM45051	Abm45051 Propionib
134	6	4.4	102	6	ABU48490	Abu48490 Protein e	207	6	4.4	161	6	ABM69602	Abm69602 Phototrab
135	6	4.4	104	4	ABG18278	Abg18278 Novel hum	208	6	4.4	162	7	ADG73103	Adg73103 Pseudomon
136	6	4.4	105	4	AAO04294	Aao04294 Human pol	209	6	4.4	162	7	ADL12158	Adl12158 Pseudomon
137	6	4.4	107	3	AAU12222	Aau12222 Zee mays	210	6	4.4	163	4	AAU47693	Aau47693 Propionib
138	6	4.4	109	4	AAO05925	Aao05925 Human pol	211	6	4.4	163	6	ABM44212	Abm44212 Propionib
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140	6	4.4	114	7	ABO33837	Ab033837 Human ant	213	6	4.4	166	6	ABP76311	Abp76311 Human GEN
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143	6	4.4	114	7	ADM41857	Adm41857 Human ant	216	6	4.4	172	4	ADG27748	Adg27748 Human nov
144	6	4.4	116	3	AAU41975	Aau41975 Human ORF	217	6	4.4	175	7	ADH87488	Adh87488 Enterococ
145	6	4.4	116	4	AAU40483	Aau40483 Propionib	218	6	4.4	176	6	ABO00445	Ab000445 Novel hum
146	6	4.4	116	6	ABM37002	Abm37002 Propionib	219	6	4.4	177	6	ABU61919	Abu61919 Mouse gly
147	6	4.4	120	4	AAU50193	Aau50193 Propionib	220	6	4.4	179	4	AAU18378	Aau18378 Human end
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149	6	4.4	120	6	ABM46712	Abm46712 Propionib	222	6	4.4	180	6	AAE32500	Aae32500 Human von
150	6	4.4	120	7	ADM41824	Adm41824 Human ant	223	6	4.4	181	4	AAU81496	Aau81496 S. epider
151	6	4.4	120	7	ADM41828	Adm41828 Human ant	224	6	4.4	181	6	ABP77694	Abp77694 N. gonorr
152	6	4.4	121	4	ABB60507	Abb60507 Drosophil	225	6	4.4	181	8	ADP08335	Adp08335 Neisseria
153	6	4.4	121	8	ADR86465	Adr86465 Aspergill	226	6	4.4	182	4	AAU39281	Aau39281 Human pol
154	6	4.4	124	7	ABE65333	Ab65333 Human pro	227	6	4.4	182	5	ABP38897	Abp38897 Staphyloc
155	6	4.4	126	3	AG41172	Ag41172 Zee mays	228	6	4.4	182	8	ADS05513	Ads05513 Staphyloc
156	6	4.4	126	4	ABG06291	Abg06291 Novel hum	229	6	4.4	183	6	ABU61914	Abu61914 Mouse gly
157	6	4.4	131	5	ABB48276	Abb48276 Listeria	230	6	4.4	183	6	ABU61913	Abu61913 Mouse gly
158	6	4.4	131	6	ABU32871	Abu32871 Protein e	231	6	4.4	183	6	ABU61918	Abu61918 Mouse gly
159	6	4.4	132	3	AAU01510	Aau01510 Human sec	232	6	4.4	183	6	ABU61915	Abu61915 Mouse gly
160	6	4.4	132	3	AAU01508	Aau01508 Human sec	233	6	4.4	183	6	ABU61917	Abu61917 Mouse gly
161	6	4.4	132	3	AAU01509	Aau01509 Human sec	234	6	4.4	183	6	ABU61916	Abu61916 Mouse gly
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163	6	4.4	135	3	AAU12221	Aau12221 Zee mays	236	6	4.4	184	7	ABO61094	Ab061094 Klebsiell
164	6	4.4	135	3	AAU06426	Aau06426 Arabidops	237	6	4.4	185	3	ABM58731	Abm58731 Breast an
165	6	4.4	135	5	ABP42709	Abp42709 Human ova	238	6	4.4	185	4	AAE03654	Aae03654 Human ext
166	6	4.4	136	4	AAU58023	Aau58023 Propionib	239	6	4.4	186	2	AAU36361	Aau36361 Fragment
167	6	4.4	136	6	ABM54542	Abm54542 Propionib	240	6	4.4	186	6	ADAI1813	Ada11813 Human nov
168	6	4.4	137	6	ABP75764	Abp75764 Human sec	241	6	4.4	187	6	ABU28580	Abu28580 Protein e
169	6	4.4	140	7	ABO67859	Ab067859 Pseudomon	242	6	4.4	188	3	ABM41929	Abm41929 Human ORF
170	6	4.4	141	2	AAW55206	Aaw55206 H. pylori	243	6	4.4	189	4	ABB11750	Abb11750 Human int
171	6	4.4	141	2	AAU01466	Aau01466 Polypepti	244	6	4.4	190	4	ABB65481	Abb65481 Drosophil

245	6	4.4	190	5	ABB07966	Abd07966 Human STU	318	6	4.4	274	6	ABU28813	Abu28813 Protein e
246	6	4.4	190	7	ADC10192	Adc10192 Human NOV	319	6	4.4	275	3	AAU24336	AAU24336 Arabidops
247	6	4.4	190	7	ADC10194	Adc10194 Human NOV	320	6	4.4	275	3	ABU63702	ABU63702 D. discoi
248	6	4.4	191	4	AAU39280	Aau39280 Human pol	321	6	4.4	275	7	ADD15785	ADD15785 Dictyoste
249	6	4.4	191	8	AAU84393	Aau84393 Human dia	322	6	4.4	275	8	ADS26432	ADS26432 Bacterial
250	6	4.4	192	4	AAU39279	Aau39279 Human pol	323	6	4.4	275	8	ADS26801	ADS26801 Bacterial
251	6	4.4	193	2	AAW55378	Aaw55378 H. pylori	324	6	4.4	276	7	ABO69260	ABO69260 Pseudomon
252	6	4.4	193	5	ABB89814	Abb89814 Human pol	325	6	4.4	276	7	ABO62892	ABO62892 Klebsiell
253	6	4.4	193	5	AAW50313	Aaw50313 Helicobac	326	6	4.4	277	5	ABP25427	ABP25427 Streptoco
254	6	4.4	193	7	ADW73116	Adw73116 Human cel	327	6	4.4	277	5	ABP25427	ABP25427 Streptoco
255	6	4.4	193	8	ADJ75651	Adj75651 Marker ge	328	6	4.4	278	4	ABG22062	ABG22062 Novel hum
256	6	4.4	194	4	AAU62234	Aau62234 Propionib	329	6	4.4	280	7	ADL22711	ADL22711 Human dis
257	6	4.4	194	6	ABM58753	Abm58753 Propionib	330	6	4.4	284	7	ADG90654	ADG90654 Hepatic s
258	6	4.4	196	7	ADC86647	Adc86647 Human GPC	331	6	4.4	285	4	AAU88340	AAU88340 Human mem
259	6	4.4	198	7	ABW74283	Abw74283 DNA clone	332	6	4.4	286	3	AAU28985	AAU28985 Arabidops
260	6	4.4	200	6	AAO19812	Aao19812 Human gem	333	6	4.4	287	5	ABW53974	ABW53974 Lactococc
261	6	4.4	203	3	AAU06232	Aau06232 Arabidops	334	6	4.4	289	4	AAU63895	AAU63895 Propionib
262	6	4.4	206	3	AAU70007	Aau70007 Human Pro	335	6	4.4	289	6	ABM60414	ABM60414 Propionib
263	6	4.4	206	8	ADK16237	Adk16237 Nanoarcha	336	6	4.4	290	8	ADS23626	ADS23626 Bacterial
264	6	4.4	207	3	AAU46926	Aau46926 Arabidops	337	6	4.4	291	7	ABO80009	ABO80009 Pseudomon
265	6	4.4	208	6	ADA33459	Ada33459 Acinetoba	338	6	4.4	292	3	AAU06230	AAU06230 Arabidops
266	6	4.4	209	3	AAU53928	Aau53928 Amino aci	339	6	4.4	292	4	AAU42102	AAU42102 Human pol
267	6	4.4	209	3	ABW21031	Abw21031 Human nuc	340	6	4.4	295	2	AAU35705	AAU35705 Chlamydia
268	6	4.4	209	4	ABW93776	Abw93776 Human pro	341	6	4.4	295	3	AAU18068	AAU18068 Arabidops
269	6	4.4	209	6	AAO19811	Aao19811 Human gem	342	6	4.4	296	3	AAU08865	AAU08865 Amino aci
270	6	4.4	209	8	ADO20059	Ado20059 Human PRO	343	6	4.4	296	4	AAU98857	AAU98857 E. coli g
271	6	4.4	209	8	ADQ09242	Adq09242 Human LOC	344	6	4.4	297	4	AAU33653	AAU33653 Pseudomon
272	6	4.4	209	8	ADP24931	Adp24931 PRO polyp	345	6	4.4	297	6	ABM70477	ABM70477 Photorhab
273	6	4.4	210	4	AAU41065	Aau41065 Human pol	346	6	4.4	297	6	ABU15572	ABU15572 Protein e
274	6	4.4	210	4	AAU41066	Aau41066 Human pol	347	6	4.4	299	2	AAU13995	AAU13995 Rape exte
275	6	4.4	210	4	AAU41067	Aau41067 Human pol	348	6	4.4	299	3	AAU42581	AAU42581 Human ORF
276	6	4.4	211	3	AAU53929	Aau53929 Amino aci	349	6	4.4	300	4	ABW70965	ABW70965 Drosophil
277	6	4.4	211	8	ABW84391	Abw84391 Human dia	350	6	4.4	301	7	ABO80025	ABO80025 Pseudomon
278	6	4.4	212	3	AAU46925	Aau46925 Arabidops	351	6	4.4	302	7	ABO62091	ABO62091 Klebsiell
279	6	4.4	215	4	AAU87344	Aau87344 Human gen	352	6	4.4	305	2	AAW53942	AAW53942 L.lactis
280	6	4.4	215	5	ABG65347	Abg65347 Human alb	353	6	4.4	305	2	AAU53945	AAU53945 L.lactis
281	6	4.4	215	6	ABR53611	AbR53611 Protein s	354	6	4.4	305	3	AAU18067	AAU18067 Arabidops
282	6	4.4	215	7	ADK64262	Adk64262 Disease t	355	6	4.4	305	8	ADQ60121	ADQ60121 Murine-de
283	6	4.4	215	7	ABO69478	AbO69478 Pseudomon	356	6	4.4	306	2	AAU86912	AAU86912 Carrot ex
284	6	4.4	215	8	ADL78614	Adl78614 Albumin f	357	6	4.4	307	3	AAU28984	AAU28984 Arabidops
285	6	4.4	216	3	AAU46924	Aau46924 Arabidops	358	6	4.4	307	5	AAU50925	AAU50925 Yeast mit
286	6	4.4	216	8	ADG19768	Adg19768 G-protein	359	6	4.4	307	8	ADS44092	ADS44092 Bacterial
287	6	4.4	218	4	AAU46504	Aau46504 Propionib	360	6	4.4	310	5	AAE18733	AAE18733 Rice NADP
288	6	4.4	218	6	ABM43023	Abm43023 Propionib	361	6	4.4	311	7	ABO66123	ABO66123 Klebsiell
289	6	4.4	218	6	ADA22701	Ada22701 A. gossyp	362	6	4.4	312	5	ABW49407	ABW49407 Listeria
290	6	4.4	219	3	AAU18069	Aau18069 Arabidops	363	6	4.4	313	2	AAU98419	AAU98419 H. pylori
291	6	4.4	222	3	AAU81517	Aau81517 S. epider	364	6	4.4	313	5	ABW49438	ABW49438 Listeria
292	6	4.4	225	7	ABO68718	AbO68718 Pseudomon	365	6	4.4	313	6	ABU32672	ABU32672 Protein e
293	6	4.4	226	4	AAU87424	Aau87424 Human gen	366	6	4.4	313	8	ADS28292	ADS28292 Bacterial
294	6	4.4	231	4	AAU30719	Aau30719 Novel hum	367	6	4.4	314	3	AAU30943	AAU30943 Arabidops
295	6	4.4	232	6	ABU40051	Abu40051 Protein e	368	6	4.4	315	4	AAU82503	AAU82503 S. epider
296	6	4.4	232	7	ABO81517	AbO81517 Pseudomon	369	6	4.4	315	5	ABW91295	ABW91295 Herbicida
297	6	4.4	233	6	ABU37916	AbU37916 Protein e	370	6	4.4	315	7	ABO81104	ABO81104 Pseudomon
298	6	4.4	234	8	ABM84392	Abm84392 Human dia	371	6	4.4	319	7	ADC95495	ADC95495 E. faeciu
299	6	4.4	235	3	AAU06231	Aau06231 Arabidops	372	6	4.4	319	8	ADH39735	ADH39735 Streptomy
300	6	4.4	241	3	AAU43660	Aau43660 Human can	373	6	4.4	321	4	ABG15289	ABG15289 Novel hum
301	6	4.4	241	6	ABU43943	Abu43943 Protein e	374	6	4.4	321	8	ADL04856	ADL04856 M. catarr
302	6	4.4	241	7	ABO69498	AbO69498 Pseudomon	375	6	4.4	324	5	ABP39235	ABP39235 Staphyloc
303	6	4.4	242	4	AAU87418	Aau87418 Human gen	376	6	4.4	324	5	ADG76328	ADG76328 Human Inc
304	6	4.4	244	7	ABO62700	AbO62700 Klebsiell	377	6	4.4	324	8	ADS05851	ADS05851 Staphyloc
305	6	4.4	245	3	AAU23927	Aau23927 Arabidops	378	6	4.4	325	4	AAU99830	AAU99830 AGC prote
306	6	4.4	248	8	ADS27183	AdS27183 Bacterial	379	6	4.4	325	5	ABU51227	ABU51227 Helicobac
307	6	4.4	250	7	ADC95110	Adc95110 E. faeciu	380	6	4.4	325	7	ADH86310	ADH86310 Enterococ
308	6	4.4	251	8	ADM06824	Adm06824 Environme	381	6	4.4	325	7	ABO83815	ABO83815 Pseudomon
309	6	4.4	253	3	AAU23926	Aau23926 Arabidops	382	6	4.4	325	8	ADJ38878	ADJ38878 MSK2 amin
310	6	4.4	254	7	ADJ69376	Adj69376 Human hea	383	6	4.4	326	3	AAU77117	AAU77117 Ebola vir
311	6	4.4	256	2	AAU37115	Aau37115 Protein i	384	6	4.4	326	7	ADJ91992	ADJ91992 Ebola vir
312	6	4.4	256	3	AAU58234	Aau58234 Arabidops	385	6	4.4	326	8	ADM48358	ADM48358 Zaire ebo
313	6	4.4	263	3	AAU38321	Abu38321 Human sec	386	6	4.4	326	8	ADM48348	ADM48348 Zaire ebo
314	6	4.4	263	6	ABU25968	Abu25968 Protein e	387	6	4.4	326	8	ADM48330	ADM48330 Zaire ebo
315	6	4.4	269	3	AAU45845	Aau45845 Arabidops	388	6	4.4	327	7	ABO63291	ABO63291 Klebsiell
316	6	4.4	269	4	ABW63951	Abw63951 Drosophil	389	6	4.4	328	3	AAU10914	AAU10914 Streptomy
317	6	4.4	270	3	AAU07532	Aau07532 Arabidops	390	6	4.4	328	3	AAU07547	AAU07547 Arabidops

391	6	4.4	329	7	ADP05714	Adf05714 Bacterial	464	6	4.4	384	5	AAE18166	Aae18166 Human mod
392	6	4.4	329	8	ADQ60123	Adq60123 His tag-T	465	6	4.4	384	5	AAE18173	Aae18173 Human mod
393	6	4.4	331	2	AAW63750	Aaw63750 A. nidula	466	6	4.4	384	5	AAE18170	Aae18170 Human mod
394	6	4.4	331	2	AAW76222	Aaw76222 Human che	467	6	4.4	384	5	AAE18171	Aae18171 Human mod
395	6	4.4	331	7	AAE39221	Aae39221 Barley NA	468	6	4.4	384	5	AAE18174	Aae18174 Human typ
396	6	4.4	331	7	ADO59263	Ado59263 Barley NA	469	6	4.4	384	5	AAE18167	Aae18167 Human typ
397	6	4.4	332	3	AAE29250	Aab29250 Barley NA	470	6	4.4	385	5	AAE18181	Aae18181 Human typ
398	6	4.4	333	3	AAE30942	Aag30942 Arabidops	471	6	4.4	385	5	AAE18179	Aae18179 Human mod
399	6	4.4	333	6	ABU26981	Abu26981 Protein e	472	6	4.4	385	5	AAE18182	Aae18182 Human mod
400	6	4.4	334	6	ABU39097	Abu39097 Protein e	473	6	4.4	385	5	AAE18184	Aae18184 Human mod
401	6	4.4	334	8	ADO43991	Ado43991 Amino aci	474	6	4.4	385	5	AAE18180	Aae18180 Human mod
402	6	4.4	334	8	ABM80630	Abm80630 Tumour-as	475	6	4.4	385	5	AAE18177	Aae18177 Human mod
403	6	4.4	334	8	ABM80629	Abm80629 Tumour-as	476	6	4.4	385	5	AAE18178	Aae18178 Human mod
404	6	4.4	337	3	AAE74311	Aay74311 Neisseria	477	6	4.4	385	5	AAE18183	Aae18183 Human typ
405	6	4.4	342	6	ABP99345	Abp99345 Orthosomy	478	6	4.4	385	5	AAE18176	Aae18176 Human mod
406	6	4.4	342	6	ABP99338	Abp99338 Orthosomy	479	6	4.4	385	7	ADH86508	Adh86508 Enterococ
407	6	4.4	342	6	ABP76722	Abp76722 Streptomy	480	6	4.4	388	8	ADN23687	Bacterial
408	6	4.4	343	5	ABM49510	Abm49510 Listeria	481	6	4.4	390	4	AAU53476	Aau53476 Propionib
409	6	4.4	343	6	ABU32875	Abu32875 Protein e	482	6	4.4	390	5	AAO21482	Aao21482 Mature hu
410	6	4.4	343	8	ADN46436	Adn46436 Thermococ	483	6	4.4	390	6	ABM49995	Abm49995 Propionib
411	6	4.4	344	6	ABU41749	Abu41749 Protein e	484	6	4.4	390	7	ADF28529	Adf28529 NGRHy mat
412	6	4.4	344	6	ABU38248	Abu38248 Protein e	485	6	4.4	390	8	ADS30198	Ads30198 Bacterial
413	6	4.4	345	6	ABR53308	Abf53308 Protein s	486	6	4.4	390	8	ADN22787	Bacterial
414	6	4.4	345	7	ADK63528	Adk63528 Disease t	487	6	4.4	394	8	ADS28248	Bacterial
415	6	4.4	345	8	ADN19182	Adn19182 Bacterial	488	6	4.4	395	2	AAR77086	Aar77086 Human sul
416	6	4.4	346	2	AAW82556	Aaw82556 Corn glyc	489	6	4.4	395	8	ADS24690	Bacterial
417	6	4.4	346	4	AAE05237	Aae05237 Corn glyc	490	6	4.4	397	2	AAW72086	Aaw72086 HSV-2 str
418	6	4.4	346	5	AAU76195	Aau76195 Corn glyc	491	6	4.4	397	4	ABG08517	Novel hum
419	6	4.4	346	7	AAE38775	Aae38775 Corn glyc	492	6	4.4	399	3	AAG28983	Aag28983 Arabidops
420	6	4.4	348	7	ABO68187	Abo68187 Pseudomon	493	6	4.4	399	6	ABU18915	Protein e
421	6	4.4	350	3	AAG47994	Aag47994 Arabidops	494	6	4.4	400	8	ADN47904	Adn47904 Thermococ
422	6	4.4	350	3	AAE08566	Aag08566 Arabidops	495	6	4.4	401	6	AAE33486	Aae33486 Human REM
423	6	4.4	350	3	AAE48006	Aag48006 Arabidops	496	6	4.4	401	7	ADE07875	Novel pro
424	6	4.4	350	6	ABM67855	Abm67855 Phototab	497	6	4.4	402	4	AAU45686	Aau45686 Propionib
425	6	4.4	350	7	ADF04333	Adf04333 Bacterial	498	6	4.4	402	6	ABM42205	Abm42205 Propionib
426	6	4.4	350	7	ABO77322	Abo77322 Pseudomon	499	6	4.4	403	8	ADS30301	Bacterial
427	6	4.4	350	8	ADN74365	Adn74365 Thale cre	500	6	4.4	403	8	ADS30152	Bacterial
428	6	4.4	351	3	AAE32579	Aag32579 Arabidops	501	6	4.4	404	7	ABO80978	AbO80978 Pseudomon
429	6	4.4	351	3	AAE48008	Aag48008 Arabidops	502	6	4.4	406	4	AAU67781	Aau67781 Propionib
430	6	4.4	351	3	AAE07379	Aag07379 Arabidops	503	6	4.4	406	6	ABM64300	Propionib
431	6	4.4	351	6	ABU18964	Abu18964 Protein e	504	6	4.4	407	7	ABO83677	AbO83677 Pseudomon
432	6	4.4	351	8	ADN74459	Adn74459 Thale cre	505	6	4.4	409	4	ABG20682	Novel hum
433	6	4.4	351	8	ADN73727	Adn73727 Thale cre	506	6	4.4	410	2	AAR10693	Aar10693 Cephalosp
434	6	4.4	353	3	AAE48005	Aag48005 Arabidops	507	6	4.4	411	7	ADE08665	Novel pro
435	6	4.4	354	3	AAE47993	Aag47993 Arabidops	508	6	4.4	416	4	AAU57642	Propionib
436	6	4.4	354	3	AAE08565	Aag08565 Arabidops	509	6	4.4	416	6	ABM54161	Abm54161 Propionib
437	6	4.4	356	3	AAE24335	Aag24335 Arabidops	510	6	4.4	416	6	ABU18455	Abu18455 Protein e
438	6	4.4	356	4	AAE79234	Aab79234 Corynebac	511	6	4.4	417	6	ABU26217	Protein e
439	6	4.4	356	4	AAE91027	Aag91027 C glutami	512	6	4.4	418	6	AAE32502	Human wil
440	6	4.4	357	4	ABG19162	Abg19162 Novel hum	513	6	4.4	418	6	ADS28776	Bacterial
441	6	4.4	358	3	AAE48007	Aag48007 Arabidops	514	6	4.4	419	8	ADM72131	Novel NTR
442	6	4.4	358	4	AAE92530	Aab92530 Human. pro	515	6	4.4	420	4	ABG13928	Abg13928 Human hum
443	6	4.4	359	3	AAE07378	Aag07378 Arabidops	516	6	4.4	420	5	AAO21477	Novel hum
444	6	4.4	359	5	ABE97563	Abb97563 Novel hum	517	6	4.4	420	6	ABR55621	Abr55621 Amino aci
445	6	4.4	362	4	AAE67309	Aab67309 ABC trans	518	6	4.4	420	7	ADF28510	Adf28510 NGRHy pre
446	6	4.4	362	8	ADO07190	Ado07190 Saccharom	519	6	4.4	420	8	ADS10516	AdS10516 Pseudomon
447	6	4.4	363	4	AAE93034	Aab93034 Human. pro	520	6	4.4	422	7	ABO72825	AbO72825 Pseudomon
448	6	4.4	363	8	ADP12978	Adp12978 Protein e	521	6	4.4	425	4	ABG24730	Abg24730 Novel hum
449	6	4.4	363	8	ADP24977	Adp24977 PRO felyp	522	6	4.4	425	7	ABO84328	AbO84328 Pseudomon
450	6	4.4	365	8	ADA34820	Ada34820 Acinetoba	523	6	4.4	427	5	ABU52159	Abu52159 Helicobac
451	6	4.4	365	8	ADS24900	Ads24900 Bacterial	524	6	4.4	427	7	ABO74603	AbO74603 Pseudomon
452	6	4.4	366	8	ADS24730	Ads24730 Bacterial	525	6	4.4	427	8	ADN21208	Adn21208 Bacterial
453	6	4.4	368	8	ADJ48378	Adj48378 Maize oil	526	6	4.4	428	4	ABG20060	Abg20060 Novel hum
454	6	4.4	369	4	AAU45721	Aau45721 Propionib	527	6	4.4	428	4	ABG20060	Abg20060 Novel hum
455	6	4.4	369	6	ABM42240	Abm42240 Propionib	528	6	4.4	428	6	ABP58648	Abp58648 Human cen
456	6	4.4	372	8	ADS44776	Ads44776 Bacterial	529	6	4.4	428	6	ABU33541	Abu33541 Protein e
457	6	4.4	376	6	ABP79804	Abp79804 N. gonorr	530	6	4.4	428	7	ADB65163	AdB65163 Human pro
458	6	4.4	378	8	ADN97130	Adn97130 ASPA01 as	531	6	4.4	433	8	ADS24137	AdS24137 Bacterial
459	6	4.4	381	7	ABO81224	AbO81224 Pseudomon	532	6	4.4	433	8	ADS27995	AdS27995 Bacterial
460	6	4.4	384	5	AAE18168	Aae18168 Human mod	533	6	4.4	434	6	ABU27232	Abu27232 Protein e
461	6	4.4	384	5	AAE18172	Aae18172 Human typ	534	6	4.4	434	6	ABU26890	Abu26890 Protein e
462	6	4.4	384	5	AAE18169	Aae18169 Human mod	535	6	4.4	436	6	ABU39822	Abu39822 Protein e
463	6	4.4	384	5	AAE18165	Aae18165 Human typ	536	6	4.4	437	7	ABO61095	AbO61095 Klebsiell

537	6	4.4	439	4	AAB96637	Aab96637 Putative	610	6	4.4	495	4	AAG90047	Aag90047 C glutami
538	6	4.4	440	5	ABB48444	Abb48444 Listeria	611	6	4.4	495	7	ADC32891	Adc32891 Human nov
539	6	4.4	441	7	ADD47749	Add47749 Human pro	612	6	4.4	495	7	ADD13447	Add13447 C. glutam
540	6	4.4	441	7	ADD47743	Add47743 Rat Prote	613	6	4.4	496	6	ABU36088	Abu36088 Protein e
541	6	4.4	441	7	ADD48842	Add48842 Rat Prote	614	6	4.4	500	6	ABM68189	Abm68189 Photorhab
542	6	4.4	441	7	ADD47747	Add47747 Rat Prote	615	6	4.4	505	7	ABO68361	AbO68361 Pseudomon
543	6	4.4	441	7	ADD47745	Add47745 Human pro	616	6	4.4	506	4	ABB58248	Abb58248 Drosophil
544	6	4.4	441	7	ADD48844	Add48844 Human pro	617	6	4.4	506	7	ADC97612	Adc97612 E. faeciu
545	6	4.4	442	7	ABO77396	AbO77396 Pseudomon	618	6	4.4	508	8	ABO79146	AbO79146 Pseudomon
546	6	4.4	443	7	ADC00947	Adc00947 Enterohae	619	6	4.4	508	8	ADN46956	Adn46956 Thermococ
547	6	4.4	445	5	ABP69674	Abp69674 Human pol	620	6	4.4	508	8	ADN20419	Adn20419 Bacterial
548	6	4.4	445	8	ADH71106	Adh71106 Human pro	621	6	4.4	510	3	AGS40249	Ags40249 Arabidops
549	6	4.4	448	5	ABP66147	Abp66147 Bifidobac	622	6	4.4	510	3	AGS39697	Ags39697 Arabidops
550	6	4.4	449	7	ABO68923	AbO68923 Pseudomon	623	6	4.4	512	8	ADS25580	AdS25580 Bacterial
551	6	4.4	451	8	ADN27135	Adn27135 Bacterial	624	6	4.4	512	8	ADS25323	AdS25323 Bacterial
552	6	4.4	452	4	ABB52566	Abb52566 Escherich	625	6	4.4	512	8	ADS26018	AdS26018 Bacterial
553	6	4.4	453	8	AQ65122	Aq65122 Novel hum	626	6	4.4	513	4	ABB65522	Abb65522 Drosophil
554	6	4.4	453	8	ADN21519	Adn21519 Bacterial	627	6	4.4	514	2	AAR05431	Aar05431 Chinese h
555	6	4.4	458	5	ABB55232	Abb55232 Lactococc	628	6	4.4	514	2	AAR05432	Aar05432 Human IMP
556	6	4.4	460	6	ADA33775	Ada33775 Actinotoba	629	6	4.4	514	4	AAB96143	Aab96143 Putative
557	6	4.4	461	6	ABP57637	Abp57637 S. muraya	630	6	4.4	514	5	AAU10695	Aau10695 Reference
558	6	4.4	461	8	ADS45016	AdS45016 Bacterial	631	6	4.4	514	5	AAE18189	Aae18189 Human wil
559	6	4.4	462	6	ABU33870	Abu33870 Protein e	632	6	4.4	514	5	AAE18186	Aae18186 Human wil
560	6	4.4	463	7	ABO69558	AbO69558 Pseudomon	633	6	4.4	514	7	ADG63316	Adg63316 Human IMP
561	6	4.4	463	7	ABO68529	AbO68529 Pseudomon	634	6	4.4	514	7	ADG63312	Adg63312 Human IMP
562	6	4.4	464	7	ABO79302	AbO79302 Pseudomon	635	6	4.4	514	7	ADG63340	Adg63340 Mouse IMP
563	6	4.4	464	7	ABO78813	AbO78813 Pseudomon	636	6	4.4	514	7	ADG63314	Adg63314 Human IMP
564	6	4.4	465	7	ABM85311	Abm85311 Human pro	637	6	4.4	514	7	ADG63320	Adg63320 Human IMP
565	6	4.4	468	4	ABM60870	Abm60870 Drosophil	638	6	4.4	514	7	ADG63318	Adg63318 Human IMP
566	6	4.4	470	4	AAAG78185	Aag78185 Mouse MIT	639	6	4.4	514	7	ADG63349	Adg63349 Human IMP
567	6	4.4	470	7	ABM85310	Abm85310 Mouse pro	640	6	4.4	514	7	ADG63310	Adg63310 Human wil
568	6	4.4	473	3	AAAY85171	Aay85171 Human MSK	641	6	4.4	514	7	ADG63338	Adg63338 Mouse wil
569	6	4.4	475	7	ADM04878	Adm04878 Human pro	642	6	4.4	514	7	ADJ68634	Adj68634 Human hea
570	6	4.4	476	6	ABU45115	Abu45115 Protein e	643	6	4.4	514	8	ADO19228	Ado19228 Human PRO
571	6	4.4	477	6	ABU36376	Abu36376 Protein e	644	6	4.4	514	8	ADP98886	Adp98886 C. albica
572	6	4.4	477	8	AQ66179	Aq66179 Novel hum	645	6	4.4	514	8	ADS88152	AdS88152 Human pro
573	6	4.4	481	2	AAR44220	Aar44220 Threonine	646	6	4.4	514	8	ADS25064	AdS25064 Bacterial
574	6	4.4	481	4	AAAB79721	Aab79721 Corynebac	647	6	4.4	515	4	ABR61379	Abr61379 Human pho
575	6	4.4	481	4	AAAG93232	Aag93232 C. glutami	648	6	4.4	515	7	ADD27826	Add27826 Human pho
576	6	4.4	481	5	ABU04679	AbJ04679 Mycobacte	649	6	4.4	515	7	ABW01496	Abw01496 Human pho
577	6	4.4	484	7	ABO67205	AbO67205 Klebsiell	650	6	4.4	515	7	ABW01545	Abw01545 Human pho
578	6	4.4	486	5	ABB47843	Abb47843 Listeria	651	6	4.4	515	7	ADJ70434	Adj70434 Human hea
579	6	4.4	487	6	ABU40885	Abu40885 Protein e	652	6	4.4	516	8	ADP09691	Adp09691 Human pro
580	6	4.4	487	8	ADJ71965	Adj71965 Human PMM	653	6	4.4	516	7	ABO73134	AbO73134 Pseudomon
581	6	4.4	487	8	ADN23458	Adn23458 Bacterial	654	6	4.4	516	7	ABO80756	AbO80756 Pseudomon
582	6	4.4	488	7	ADF06666	Adf06666 Bacterial	655	6	4.4	517	3	ABG46195	Abg46195 Arabidops
583	6	4.4	489	3	AAAG40251	Aag40251 Arabidops	656	6	4.4	518	2	AAW67616	Aaw67616 A. nidula
584	6	4.4	489	7	ABO69831	AbO69831 Pseudomon	657	6	4.4	519	7	ABO65074	AbO65074 Klebsiell
585	6	4.4	490	8	ADO20015	Ado20015 Human PRO	658	6	4.4	520	7	ABO83759	AbO83759 Pseudomon
586	6	4.4	490	8	ADR14043	Adr14043 Human NP-	659	6	4.4	523	7	ADK62490	Adk62490 Disease t
587	6	4.4	491	3	AG40250	Aag40250 Arabidops	660	6	4.4	523	8	ADS43504	AdS43504 Bacterial
588	6	4.4	491	4	AAU38486	Aau38486 Salmonell	661	6	4.4	523	8	ADS22445	AdS22445 Bacterial
589	6	4.4	491	4	AAU34439	Aau34439 E. coli c	662	6	4.4	526	7	ABM85867	Abm85867 Human pro
590	6	4.4	491	4	AAAG98407	Aag98407 Escherich	663	6	4.4	527	7	ABO68450	AbO68450 Pseudomon
591	6	4.4	491	6	ABU27754	Abu27754 Protein e	664	6	4.4	527	8	ADP99173	Adp99173 Human tra
592	6	4.4	491	6	ABU48098	Abu48098 Protein e	665	6	4.4	528	7	ABO71167	AbO71167 Pseudomon
593	6	4.4	491	6	ABU31655	Abu31655 Protein e	666	6	4.4	529	7	ADH88063	Adh88063 Enterococ
594	6	4.4	491	6	ABU50003	Abu50003 Protein e	667	6	4.4	529	8	ADN21539	Adn21539 Bacterial
595	6	4.4	491	6	ABU47266	Abu47266 Protein e	668	6	4.4	529	8	ADR66377	Adr66377 Human pro
596	6	4.4	491	6	ADU28492	Adu28492 Protein e	669	6	4.4	529	8	ADR66719	Adr66719 Human pro
597	6	4.4	491	7	ADL46386	Adl46386 UDP-N-ace	670	6	4.4	531	7	ABO73763	AbO73763 Pseudomon
598	6	4.4	491	7	ADL46388	Adl46388 UDP-N-ace	671	6	4.4	532	7	ABO70495	AbO70495 Pseudomon
599	6	4.4	492	4	ABR61385	AbR61385 Murine ph	672	6	4.4	533	8	ADN22745	Adn22745 Bacterial
600	6	4.4	492	6	ABM68866	Abm68866 Photorhab	673	6	4.4	534	7	ABO78554	AbO78554 Pseudomon
601	6	4.4	492	7	ADD27828	Add27828 Mouse pho	674	6	4.4	535	6	ABU15732	Abu15732 Protein e
602	6	4.4	492	7	ABW01497	Abw01497 Murine ph	675	6	4.4	535	6	AAO24109	Aao24109 M acetivo
603	6	4.4	492	7	ABW01546	Abw01546 Murine ph	676	6	4.4	536	4	ABG13708	Abg13708 Novel hum
604	6	4.4	492	7	ADL65715	Adl65715 C. glutam	677	6	4.4	536	7	ADB66953	AdB66953 E. coli K
605	6	4.4	492	7	ABO65763	AbO65763 Klebsiell	678	6	4.4	536	7	ADC31190	AdC31190 Human nov
606	6	4.4	493	2	AAW55517	Aaw55517 H. pylori	679	6	4.4	540	7	ADD25637	Add25637 Binding d
607	6	4.4	493	5	AAW50311	Aam50311 Helicobac	680	6	4.4	542	4	ABG13709	Abg13709 Novel hum
608	6	4.4	494	7	ADF05705	Adf05705 Bacterial	681	6	4.4	544	6	ABR53439	AbR53439 Protein s
609	6	4.4	495	1	AAAP81325	Aap81325 Threonine	682	6	4.4	544	7	ADK64646	AdK64646 Disease t

683	6	4.4	545	4	AAB65649	Aab65649 Novel pro	756	6	4.4	618	5	AAO21865	Aao21865 Isoprenoi
684	6	4.4	545	8	ADI29256	Adi29256 Human MAR	757	6	4.4	619	4	AAM41661	Aam41661 Human pol
685	6	4.4	546	7	ADK65863	Adk65863 Extensin-	758	6	4.4	623	8	ADN24795	Adn24795 Bacterial
686	6	4.4	550	6	ABM68260	Abm68260 Phototab	759	6	4.4	623	8	ADN22036	Adn22036 Bacterial
687	6	4.4	550	8	ADM80085	Adm80085 Spiramyci	760	6	4.4	630	6	ABJ75392	Abj75392 Aspergill
688	6	4.4	550	8	ADN97601	Adn97601 S ambofac	761	6	4.4	636	6	ABM65172	Abm65172 Propionib
689	6	4.4	551	6	ABU38501	Abu38501 Protein e	762	6	4.4	637	5	ABB93928	Abb93928 Herbicida
690	6	4.4	551	6	ABU41945	Abu41945 Protein e	763	6	4.4	638	6	ABU50354	Abu50354 Protein e
691	6	4.4	551	8	ADS26035	Ads26035 Bacterial	764	6	4.4	639	5	ABB97389	Abb97389 Novel hum
692	6	4.4	552	6	ABR53246	AbR53246 Protein s	765	6	4.4	640	4	AAE09481	Aae09481 Mouse int
693	6	4.4	552	7	ADK36668	Adk36668 Disease t	766	6	4.4	642	6	ABU16881	Abu16881 Protein e
694	6	4.4	553	4	AAE04897	Aae04897 Human tra	767	6	4.4	642	7	ABO83358	AbO83358 Pseudomon
695	6	4.4	553	5	AAU98944	Aau98944 Human 553	768	6	4.4	663	8	ADS26595	Ads26595 Bacterial
696	6	4.4	553	7	ADE82896	Ade82896 Human sul	769	6	4.4	663	8	ADS26970	Ads26970 Bacterial
697	6	4.4	554	4	AAB47275	AbA47275 hOAT4. 8/	770	6	4.4	664	4	AAA67308	Aaa67308 ABC trans
698	6	4.4	554	6	ABU40202	Abu40202 Protein e	771	6	4.4	664	6	ADA35769	Ada35769 Acinetoba
699	6	4.4	557	8	ADM80084	Adm80084 Spiramyci	772	6	4.4	667	6	ABU44138	Abu44138 Protein e
700	6	4.4	557	8	ADN97600	Adn97600 S ambofac	773	6	4.4	671	6	ABU20436	Abu20436 Protein e
701	6	4.4	557	8	ADS25335	Ads25335 Bacterial	774	6	4.4	671	7	ABO83116	AbO83116 Pseudomon
702	6	4.4	558	7	ADM05589	Adm05589 Human pro	775	6	4.4	679	2	AAR69870	Aar69870 Oncorhync
703	6	4.4	559	2	AAW50909	Aaw50909 Alteromon	776	6	4.4	679	2	AAR69868	Aar69868 Oncorhync
704	6	4.4	559	3	AAG29748	Aag29748 Arabidops	777	6	4.4	679	7	ADM25673	Adm25673 Hyperther
705	6	4.4	560	3	AAE42058	Aae42058 Human ORF	778	6	4.4	680	2	AAR69869	Aar69869 Oncorhync
706	6	4.4	560	8	ADS25588	Ads25588 Bacterial	779	6	4.4	680	2	AAR69871	Aar69871 Oncorhync
707	6	4.4	561	2	AAW98552	Aaw98552 H. pylori	780	6	4.4	680	3	AGA46193	AgA46193 Arabidops
708	6	4.4	561	4	ABG09019	Abg09019 Novel hum	781	6	4.4	686	4	AAB85339	Aab85339 Human sem
709	6	4.4	562	2	AAU06429	Aau06429 Human mat	782	6	4.4	692	7	ABO79251	AbO79251 Pseudomon
710	6	4.4	562	4	AAU33507	Aau33507 Enterococ	783	6	4.4	694	3	AAG29747	AgA29747 Arabidops
711	6	4.4	562	4	AAE85160	Aae85160 Matrix me	784	6	4.4	694	8	ADO61597	AdO61597 Transcript
712	6	4.4	563	2	AAU06428	Aau06428 Human mat	785	6	4.4	695	7	ADM05114	Adm05114 Human pro
713	6	4.4	563	4	ABR93328	AbR93328 Human pro	786	6	4.4	696	2	AAW55698	Aaw55698 H. pylori
714	6	4.4	563	4	ABP69374	Abp69374 Human pol	787	6	4.4	696	2	AAU17207	Aay17207 H. pylori
715	6	4.4	565	5	AAE31063	Aae31063 Ehrlichia	788	6	4.4	696	5	AAM50309	Aam50309 Helicobac
716	6	4.4	565	6	AAO19624	Aao19624 Human nox	789	6	4.4	696	5	AAW50310	Aaw50310 Helicobac
717	6	4.4	565	8	ADG62954	Adg62954 Nox5. 3/2	790	6	4.4	699	5	ABG93041	Abg93041 S. cerevi
718	6	4.4	565	8	ADJ75251	Adj75251 Human NOX	791	6	4.4	699	6	ABJ25992	Abj25992 Aspergill
719	6	4.4	568	8	ADS21843	Ads21843 Bacterial	792	6	4.4	699	8	ADN18777	Adn18777 Bacterial
720	6	4.4	572	4	AAU35140	Aau35140 Enterococ	793	6	4.4	705	3	AAW85169	Aay85169 Microgen a
721	6	4.4	572	6	ABU14582	Abu14582 Protein e	794	6	4.4	705	7	ABO73430	AbO73430 Pseudomon
722	6	4.4	572	8	ADS43544	Ads43544 Bacterial	795	6	4.4	706	6	ABU48763	Abu48763 Protein e
723	6	4.4	573	7	ADB80097	Adb80097 Mycobacte	796	6	4.4	708	8	ADP30092	Adp30092 Human sec
724	6	4.4	577	6	ABU22594	Abu22594 Protein e	797	6	4.4	710	7	ADC31663	Adc31663 Human nov
725	6	4.4	578	4	ABB59765	Abb59765 Drosophil	798	6	4.4	710	8	ADQ65698	Adq65698 Novel hum
726	6	4.4	581	8	ADL05053	Adl05053 M. catarr	799	6	4.4	711	3	AAW85170	Aay85170 MS2 spli
727	6	4.4	582	8	ADM80083	Adm80083 Spiramyci	800	6	4.4	713	8	ADS23614	Ads23614 Bacterial
728	6	4.4	582	8	ADN97599	Adn97599 S ambofac	801	6	4.4	720	7	ABO83169	AbO83169 Pseudomon
729	6	4.4	584	4	ABG21351	Abg21351 Novel hum	802	6	4.4	721	2	AAW72211	Aaw72211 HSV-2 str
730	6	4.4	592	7	ABO69726	AbO69726 Pseudomon	803	6	4.4	722	5	AAE17810	Aae17810 Herpes si
731	6	4.4	592	8	ADN25834	Adn25834 Bacterial	804	6	4.4	722	7	ADG74943	Adg74943 Human her
732	6	4.4	595	4	ABG30102	Abg30102 Novel hum	805	6	4.4	722	7	ADG75163	Adg75163 Human her
733	6	4.4	599	7	ABO68504	AbO68504 Pseudomon	806	6	4.4	722	7	ADG75087	Adg75087 Human her
734	6	4.4	601	3	AAU90851	Aau90851 Castor be	807	6	4.4	722	8	ADJ77801	Adj77801 Herpes si
735	6	4.4	601	7	ABO81843	AbO81843 Pseudomon	808	6	4.4	726	6	ABR53052	AbR53052 Protein s
736	6	4.4	605	2	AAO39923	Aao39923 Bacillus	809	6	4.4	726	6	ADK62916	Adk62916 Disease t
737	6	4.4	605	6	ABU34329	Abu34329 Protein e	810	6	4.4	726	7	ABO79773	AbO79773 Pseudomon
738	6	4.4	605	8	ADJ49552	Adj49552 Oii-assoc	811	6	4.4	733	8	ABM83597	Abm83597 Human dia
739	6	4.4	606	4	AAU39875	Aau39875 Human pol	812	6	4.4	738	8	ADN19789	Adn19789 Bacterial
740	6	4.4	607	8	ADS30440	Ads30440 Bacterial	813	6	4.4	739	6	AAE33189	Aae33189 Human LfE
741	6	4.4	608	8	ADN20934	Adn20934 Bacterial	814	6	4.4	739	6	ABU62391	Abu62391 Leucine z
742	6	4.4	610	5	ABG80347	Abg80347 Clostridi	815	6	4.4	739	7	ADC31806	Adc31806 Human nov
743	6	4.4	611	6	ABU17571	Abu17571 Protein e	816	6	4.4	739	7	ADJ68968	Adj68968 Human hea
744	6	4.4	611	8	ADJ49585	Adj49585 Oii-assoc	817	6	4.4	739	7	ADJ68969	Adj68969 Human hea
745	6	4.4	612	4	ABB58181	Abb58181 Drosophil	818	6	4.4	739	8	ADN19863	Adn19863 Bacterial
746	6	4.4	612	7	ADF74755	Adf74755 Murine dn	819	6	4.4	752	4	AAU34688	Aau34688 E. coli c
747	6	4.4	612	7	ABO76981	AbO76981 Pseudomon	820	6	4.4	752	6	ABU15119	Abu15119 Protein e
748	6	4.4	612	8	ADR10271	AdR10271 Human pro	821	6	4.4	757	4	ABB66427	Abb66427 Drosophil
749	6	4.4	613	4	AAW95548	Aaw95548 Human pro	822	6	4.4	762	7	ABO63491	AbO63491 Klebsiell
750	6	4.4	613	4	AAW94035	Aaw94035 Human sto	823	6	4.4	772	2	AAR70690	Aar70690 Mesquite
751	6	4.4	614	7	ABO79884	AbO79884 Pseudomon	824	6	4.4	772	3	AAW85175	Aay85175 Mitogen a
752	6	4.4	614	8	ADN23263	Adn23263 Bacterial	825	6	4.4	772	8	ADQ15048	Adq15048 Human can
753	6	4.4	614	8	ADN23262	Adn23262 Bacterial	826	6	4.4	776	3	AAW96167	Aay96167 Schizosac
754	6	4.4	615	8	ADS27325	Ads27325 Bacterial	827	6	4.4	784	5	ABG70086	Abg70086 Human pre
755	6	4.4	617	3	AAG46194	Aag46194 Arabidops	828	6	4.4	784	5	ABP68598	Abp68598 Human pan

829	6	4.4	785	4	AAB94320	Human pro	Aab94320	Human pro	902	6	4.4	888	6	ADB26989	Human PRO
830	6	4.4	785	6	ABU69617	Human NP-	Abu69617	Human NP-	903	6	4.4	888	6	ADB31276	Human PRO
831	6	4.4	785	7	ADJ69241	Human hea	Adj69241	Human hea	904	6	4.4	888	6	ADA61204	Homo sapi
832	6	4.4	788	8	ABW83596	Human dia	Abw83596	Human dia	905	6	4.4	888	6	ADB24351	Human PRO
833	6	4.4	789	8	ADC43700	Bacterial	Adc43700	Bacterial	906	6	4.4	888	6	ADA96680	Human PRO
834	6	4.4	793	7	ADC03400	Rice flow	Adc03400	Rice flow	907	6	4.4	888	6	ADA81252	Human PRO
835	6	4.4	794	4	AMW79803	Human pro	Aam79803	Human pro	908	6	4.4	888	6	ADA96128	Human PRO
836	6	4.4	794	7	ADB70250	C. neofo	Adb70250	C. neofo	909	6	4.4	888	6	ADB26437	Human PRO
837	6	4.4	798	8	ADA42567	Bacterial	Ada42567	Bacterial	910	6	4.4	888	6	ADB21922	Novel hum
838	6	4.4	807	4	ABG15173	Novel hum	Abg15173	Novel hum	911	6	4.4	888	7	ADA77701	Human PRO
839	6	4.4	807	8	ADT72097	Amino aci	Adt72097	Amino aci	912	6	4.4	888	7	ADB18441	Human PRO
840	6	4.4	815	7	ADM05553	Human pro	Adm05553	Human pro	913	6	4.4	888	7	ADA87124	Novel hum
841	6	4.4	816	7	ADC03488	Rice flow	Adc03488	Rice flow	914	6	4.4	888	7	ABO25134	Human sec
842	6	4.4	822	7	ADB70257	C. neofo	Adb70257	C. neofo	915	6	4.4	888	7	ADA88227	Novel hum
843	6	4.4	832	5	ABP35689	Fungal ZB	Abp35689	Fungal ZB	916	6	4.4	888	7	ADA88227	Novel hum
844	6	4.4	832	8	ADN18887	Bacterial	Adn18887	Bacterial	917	6	4.4	888	7	ADB28645	Human PRO
845	6	4.4	835	4	AMW78819	Human pro	Aam78819	Human pro	918	6	4.4	888	7	ADB23197	Human PRO
846	6	4.4	837	8	ADS29553	Bacterial	Ads29553	Bacterial	919	6	4.4	888	7	ADA77149	Human PRO
847	6	4.4	842	1	ADP93712	Sequence	Adp93712	Sequence	920	6	4.4	888	7	ADA88779	Human PRO
848	6	4.4	849	4	ABG15965	Novel hum	Abg15965	Novel hum	921	6	4.4	888	7	ADA97784	Human PRO
849	6	4.4	852	6	ABU29140	Protein e	Abu29140	Protein e	922	6	4.4	888	7	ADB27541	Human PRO
850	6	4.4	854	2	AAW19857	Human sem	Aaw19857	Human sem	923	6	4.4	888	7	ADB22474	Novel hum
851	6	4.4	888	3	AB18916	A novel p	Ab18916	A novel p	924	6	4.4	888	7	ADA67165	Human PRO
852	6	4.4	888	4	AAU12443	Human PRO	Aau12443	Human PRO	925	6	4.4	888	7	ADB23026	Human PRO
853	6	4.4	888	5	ABB84950	Human PRO	Abb84950	Human PRO	926	6	4.4	888	7	ADB23799	Human PRO
854	6	4.4	888	5	ABB95556	Human ang	Abb95556	Human ang	927	6	4.4	888	7	ADA92521	Novel hum
855	6	4.4	888	6	ABU03538	Angiogene	Abu03538	Angiogene	928	6	4.4	888	7	ADB15584	Human PRO
856	6	4.4	888	6	ABO17887	Novel hum	Ab017887	Novel hum	929	6	4.4	888	7	ADB38836	Novel hum
857	6	4.4	888	6	ABU69110	Human PRO	Abu69110	Human PRO	930	6	4.4	888	7	ADB38284	Novel hum
858	6	4.4	888	6	ABU81141	Human PRO	Abu81141	Human PRO	931	6	4.4	888	7	ADB6756	Novel hum
859	6	4.4	888	6	ABO19426	Human sec	Ab019426	Human sec	932	6	4.4	888	7	ADB89836	Human PRO
860	6	4.4	888	6	ABU66841	Human PRO	Abu66841	Human PRO	933	6	4.4	888	7	ADB90568	Human PRO
861	6	4.4	888	6	ABU59922	Novel sec	Abu59922	Novel sec	934	6	4.4	888	7	ADB39669	Novel hum
862	6	4.4	888	6	ABU69087	Human PRO	Abu69087	Human PRO	935	6	4.4	888	7	ADB47292	Novel hum
863	6	4.4	888	6	ABO25112	Human sec	Ab025112	Human sec	936	6	4.4	888	7	ADB86899	Human PRO
864	6	4.4	888	6	ABU67117	Human sec	Abu67117	Human sec	937	6	4.4	888	7	ADB77504	Novel hum
865	6	4.4	888	6	ABU81551	Human sec	Abu81551	Human sec	938	6	4.4	888	7	ADB34661	Human PRO
866	6	4.4	888	6	ADA46063	Novel hum	Ada46063	Novel hum	939	6	4.4	888	7	ADB35765	Human PRO
867	6	4.4	888	6	ADA76560	Novel hum	Ada76560	Novel hum	940	6	4.4	888	7	ADB334109	Human PRO
868	6	4.4	888	6	ADA76494	Human PRO	Ada76494	Human PRO	941	6	4.4	888	7	ADB35213	Human PRO
869	6	4.4	888	6	ADA19144	Human PRO	Ada19144	Human PRO	942	6	4.4	888	7	ADB36317	Novel hum
870	6	4.4	888	6	ADA61767	Homo sapi	Ada61767	Homo sapi	943	6	4.4	888	7	ADB46712	Novel hum
871	6	4.4	888	6	ADB19552	Novel hum	Adb19552	Novel hum	944	6	4.4	888	7	AAE39104	Human PRO
872	6	4.4	888	6	ADB28093	Human PRO	Adb28093	Human PRO	945	6	4.4	888	7	AAE39041	Human PRO
873	6	4.4	888	6	ADA86572	Novel hum	Ada86572	Novel hum	946	6	4.4	888	7	ADC50585	Novel hum
874	6	4.4	888	6	ADB16136	Human PRO	Adb16136	Human PRO	947	6	4.4	888	7	ADC72132	Novel hum
875	6	4.4	888	6	ADA47922	Human PRO	Ada47922	Human PRO	948	6	4.4	888	7	ADC29791	Novel hum
876	6	4.4	888	6	ADA67717	Human PRO	Ada67717	Human PRO	949	6	4.4	888	7	ADC60111	Novel hum
877	6	4.4	888	6	ADB30724	Human PRO	Adb30724	Human PRO	950	6	4.4	888	7	ADC53118	Novel hum
878	6	4.4	888	6	ADA86020	Novel hum	Ada86020	Novel hum	951	6	4.4	888	7	ADC57472	Novel hum
879	6	4.4	888	6	ADA97232	Human PRO	Ada97232	Human PRO	952	6	4.4	888	7	ADC60663	Novel hum
880	6	4.4	888	6	ADA79536	Human PRO	Ada79536	Human PRO	953	6	4.4	888	7	ADC51138	Novel hum
881	6	4.4	888	6	ADA87675	Novel hum	Ada87675	Novel hum	954	6	4.4	888	7	ADC65665	Human PRO
882	6	4.4	888	6	ADB16877	Human PRO	Adb16877	Human PRO	955	6	4.4	888	7	ADC54763	Novel hum
883	6	4.4	888	6	ADA91969	Novel hum	Ada91969	Novel hum	956	6	4.4	888	7	ADC53724	Novel hum
884	6	4.4	888	6	ADB15032	Human PRO	Adb15032	Human PRO	957	6	4.4	888	7	ADC59247	Novel hum
885	6	4.4	888	6	ADB18993	Novel hum	Adb18993	Novel hum	958	6	4.4	888	7	ADC56125	Novel hum
886	6	4.4	888	6	ADA94208	Human PRO	Ada94208	Human PRO	959	6	4.4	888	7	ADC38695	Novel hum
887	6	4.4	888	6	ADB20104	Novel hum	Adb20104	Novel hum	960	6	4.4	888	7	ADD03369	Novel hum
888	6	4.4	888	6	ADB13416	Human PRO	Adb13416	Human PRO	961	6	4.4	888	7	ADC90361	Novel hum
889	6	4.4	888	6	ABO43420	Novel hum	Ab043420	Novel hum	962	6	4.4	888	7	ADC69780	Human PRO
890	6	4.4	888	6	ADA74670	Human PRO	Ada74670	Human PRO	963	6	4.4	888	7	ADC48669	Human PRO
891	6	4.4	888	6	ADB24903	Human PRO	Adb24903	Human PRO	964	6	4.4	888	7	ADD10198	Human PRO
892	6	4.4	888	6	ADA82427	Human PRO	Ada82427	Human PRO	965	6	4.4	888	7	ADD04773	Novel hum
893	6	4.4	888	6	ADA75390	Human PRO	Ada75390	Human PRO	966	6	4.4	888	7	ADC80729	Novel hum
894	6	4.4	888	6	ADA85468	Novel hum	Ada85468	Novel hum	967	6	4.4	888	7	ADD11236	Human PRO
895	6	4.4	888	6	ADA84916	Novel hum	Ada84916	Novel hum	968	6	4.4	888	7	ADD10557	Human sec
896	6	4.4	888	6	ADB30172	Human PRO	Adb30172	Human PRO	969	6	4.4	888	7	ADC48117	Human PRO
897	6	4.4	888	6	ADA80700	Human PRO	Ada80700	Human PRO	970	6	4.4	888	7	ADC80177	Novel hum
898	6	4.4	888	6	ADA75942	Human PRO	Ada75942	Human PRO	971	6	4.4	888	7	ADD11517	Human sec
899	6	4.4	888	6	ADA47167	Human PRO	Ada47167	Human PRO	972	6	4.4	888	7	ADD09646	Human PRO
900	6	4.4	888	6	ADB25463	Human PRO	Adb25463	Human PRO	973	6	4.4	888	7	ADD41359	Novel hum
901	6	4.4	888	6	ADA93639	Human PRO	Ada93639	Human PRO	974	6	4.4	888	7	ADD52498	Human PRO

XX PS Claim 4; Page 133-134; 156pp; English.

XX CC The present sequence is human TRAF7 TRAF (tumour necrosis factor, TNF

CC receptor-associated factor)-protein binding domain (TPBD) protein. TPBDs

CC and/or anti-TPBD antibodies (Ab) are used to identify agents for

CC treatment of autoimmune diseases, inflammation, allergy, allograft

CC rejection, sepsis, cancers such as gliomas, carcinomas, adenocarcinomas,

CC sarcomas, melanomas, hamartomas, leukaemias and lymphomas, benign

CC proliferative diseases, benign prostatic hyperplasia, keratinocyte

CC hyperplasia, neoplasia, keloid, inflammatory hyperplasia, fibrosis,

CC smooth muscle cell proliferation in arteries following balloon

CC angioplasty (restenosis), bone marrow aplasia or generally any condition

CC that involves abnormal apoptosis, cellular proliferation, differentiation

CC or stress responses or immunoglobulin class switching in B cells. Agents

CC (Ab or oligonucleotides) that bind specifically to TPBD or its nucleic

CC acid are useful for diagnosis of the specified diseases, particularly for

CC diagnosis or prognosis of cancer or for monitoring therapy

XX SQ Sequence 153 AA;

Query Match 100.0%; Score 135; DB 4; Length 153;

Best Local Similarity 100.0%; Pred. No. 4e-133;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGRGYLSVPLE 60

Db 4 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGRGYLSVPLE 63

Qy 61 LSAGLPETSKYRYRVEVMVHQSCNDPTKNI IREFASDFEVCWCYNRFFRLDLLANEGYL 120

Db 64 LSAGLPETSKYRYRVEVMVHQSCNDPTKNI IREFASDFEVCWCYNRFFRLDLLANEGYL 123

Qy 121 NPQNDTVILRFQVRS 135

Db 124 NPQNDTVILRFQVRS 138

RESULT 3

AAAM39261

ID AAAM39261 standard; protein; 964 AA.

AC AAAM39261;

XX 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2406.

XX Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren P, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AAI58417.

XX Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.

XX Example 4; SEQ ID NO 2406; 10078pp; English.

PS The invention relates to human nucleic acids (AAI57798-AAI61369) and the

XX encoded polypeptides (AAM38642-RAAM42213) with nontropic.

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders. Note: The sequence data for this patent did not form

CC part of the printed specification

XX SQ Sequence 964 AA;

Query Match 100.0%; Score 135; DB 4; Length 964;

Best Local Similarity 100.0%; Pred. No. 2.3e-132;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGRGYLSVPLE 60

Db 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGRGYLSVPLE 330

Qy 61 LSAGLPETSKYRYRVEVMVHQSCNDPTKNI IREFASDFEVCWCYNRFFRLDLLANEGYL 120

Db 331 LSAGLPETSKYRYRVEVMVHQSCNDPTKNI IREFASDFEVCWCYNRFFRLDLLANEGYL 390

Qy 121 NPQNDTVILRFQVRS 135

Db 391 NPQNDTVILRFQVRS 405

RESULT 4

ABU03763

ID ABU03763 standard; protein; 964 AA.

XX ABU03763;

AC 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #429.

DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

XX protease; protease inhibitor; transporter; cytoskeletal protein;

KW receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;

KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

OS WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX

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PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
PA
XX Chiciz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 429; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 964 AA;
XX
XX Query Match 100.0%; Score 135; DB 6; Length 964;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-132;
XX Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSVFL 60
XX Db 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSVFL 330
XX
XX QY 61 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIRFASDFEVCWCYGNRFFRLDLLANEGYL 120
XX Db 331 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIRFASDFEVCWCYGNRFFRLDLLANEGYL 390
XX
XX QY 121 NPQNDTVILRFQVRS 135
XX Db 391 NPQNDTVILRFQVRS 405
XX
XX RESULT 5
XX ID ABU03765
XX AC ABU03765;
XX XX 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #431.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX XX WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX XX (ZYCO-) ZYCOS INC.
XX PA
XX Chiciz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 431; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 964 AA;
XX
XX Query Match 100.0%; Score 135; DB 6; Length 964;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-132;
XX Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSVFL 60
XX Db 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSVFL 330
XX
XX QY 61 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIRFASDFEVCWCYGNRFFRLDLLANEGYL 120
XX Db 331 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIRFASDFEVCWCYGNRFFRLDLLANEGYL 390
XX
XX QY 121 NPQNDTVILRFQVRS 135
XX Db 391 NPQNDTVILRFQVRS 405
XX
XX RESULT 6
XX ID ABU03758
XX AC ABU03758;
XX XX 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #431.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

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DE Human expressed protein tag (EPT) #424.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

XX protease; protease inhibitor; transporter; cytoskeletal protein;

KW receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;

KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,

PT cytoskeletal proteins, receptors or transcription factors), useful for

PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

PT leukemia.

XX Example 2; SEQ ID NO 424; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a

CC fragment of a kinase, phosphatase, protease, protease inhibitor,

CC transporter, cytoskeletal protein, receptor or transcription factor. The

CC polypeptide is useful as an immunogenic composition for eliciting in a

CC mammal an immunogenic response directed against any of the purified

CC polypeptide. The purified polypeptide, or the antibody that binds to this

CC polypeptide, is useful for treating cancer. The polypeptide is also

CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and

CC polynucleotides are particularly useful for treating or preventing

CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukaemia. These are also useful for screening agents for

CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed

CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 964 AA;

Query Match 100.0%; Score 135; DB 6; Length 964;

Best Local Similarity 100.0%; Pred. No. 2.3e-132;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSTFVLENFSTRQADPVYSPPLQVSGLCWRLKVPYDNGVWRGYLSVLE 60

Db 271 ELVPSYDSTFVLENFSTRQADPVYSPPLQVSGLCWRLKVPYDNGVWRGYLSVLE 330

Qy 61 LSAGLPETSKYRYVEMVHQSCNDPTKNIREFASDFVEGCGVYRFRLLDLANEGYL 120

Db 331 LSAGLPETSKYRYVEMVHQSCNDPTKNIREFASDFVEGCGVYRFRLLDLANEGYL 390

Qy 121 NPQNDTVILRFQVRS 135

Db 391 NPQNDTVILRFQVRS 405

RESULT 7

AAB41571

ID AAB41571 standard; protein; 979 AA.

XX AAB41571;

AC AAB41571;

XX 08-FEB-2001 (first entry)

DT DT

XX Human ORFX ORF1335 polypeptide sequence SEQ ID NO:2670.

DE Human; open reading frame; ORFX; detection; cytotactic; hepatotropic;

KW vulnary; antipsoriatic; antiparkinsonian; neuroprotective;

KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;

KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;

KW hypotensive; dermatological; immunosuppressive; antinflammatory;

KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;

KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;

KW neurodegenerative disorder; osteoarthritis; graft vs host disease;

KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

KW cholesterol ester storage; systemic lupus erythematosus; infection;

KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

KW bone damage; cartilage damage; antinflammatory disease; coagulation;

KW thrombosis; contraceptive.

XX Homo sapiens.

OS WO200058473-A2.

XX 05-OCT-2000.

PD 31-MAR-2000; 2000WO-US008621.

XX 31-MAR-1999; 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach M;

PI WPI; 2000-602362/57.

XX N-PSDB; AAC75780.

DR Novel nucleic acids and peptides derived from open reading frame X,

XX useful for treating e.g. cancers, proliferative disorders,

XX neurodegenerative disorders and cardiovascular disease.

Claim 11; Page 1914-1916; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,

which represent the human ORFX open reading frames 1 to 3161. The ORFX

sequences have activities such as: cytotactic; hepatotropic; vulnary;

antipsoriatic; antiparkinsonian; neuroprotective; osteopathic;

anticonvulsant; antirheumatic; immunosuppressant; immunostimulant;

cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;

dermatological; immunosuppressive; antinflammatory; antibacterial;

antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The

sequences can be used for determining the presence of or predisposition

to, or preventing or treating pathological conditions associated with an

ORFX-associated disorder. The nucleic acids can be used to express ORFX

proteins in gene therapy vectors. The proteins and nucleic acids may be

used to treat cancers, proliferative disorders, neurodegenerative

disorders, osteoarthritis, graft vs host disease, cardiovascular disease,

diabetes mellitus, hypertension, hypothyroidism, cholesterol ester

storage, systemic lupus erythematosus, severe combined immunodeficiency

(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune

disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and

cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to

enhance coagulation; to inhibit thrombosis; and as a contraceptive

Sequence 979 AA;


```
PA (ZYCO-) ZYCOS INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 432; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 979 AA;
SQ
Query Match 100.0%; Score 135; DB 6; Length 979;
Best Local Similarity 100.0%; Pred. No. 2.3e-132;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPDNGVVRGYLSVPLE 60
DB 286 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPDNGVVRGYLSVPLE 345
QY 61 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWGYNRRFRDLLEANEGYL 120
DB 346 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWGYNRRFRDLLEANEGYL 405
QY 121 NPQNDTVILRFQVRS 135
DB 406 NPQNDTVILRFQVRS 420
RESULT 10
ABU03757
ID ABU03757 standard; protein; 979 AA.
XX
XX ABU03757;
AC
XX
XX 29-JAN-2003 (first entry)
DT
XX
XX Human expressed protein tag (EPT) #423.
DE
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
OS
XX
XX WO200278524-A2.
PN
XX
XX 10-OCT-2002.
PD
XX
XX 28-MAR-2002; 2002WO-US009671.
PF
```

```
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 423; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 979 AA;
SQ
Query Match 100.0%; Score 135; DB 6; Length 979;
Best Local Similarity 100.0%; Pred. No. 2.3e-132;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPDNGVVRGYLSVPLE 60
DB 286 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPDNGVVRGYLSVPLE 345
QY 61 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWGYNRRFRDLLEANEGYL 120
DB 346 LSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWGYNRRFRDLLEANEGYL 405
QY 121 NPQNDTVILRFQVRS 135
DB 406 NPQNDTVILRFQVRS 420
RESULT 11
ABU03759
ID ABU03759 standard; protein; 979 AA.
XX
XX ABU03759;
AC
XX
XX 29-JAN-2003 (first entry)
DT
XX
XX Human expressed protein tag (EPT) #425.
DE
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
```


61 LSAGLPETSKYEVVMVHQSCNDPTKNI IREFASDFVGCWGYNRRFRDLNLLANEGYL 120
 346 LSAGLPETSKYEVVMVHQSCNDPTKNI IREFASDFVGCWGYNRRFRDLNLLANEGYL 405
 QY 121 NPQNDTVILRFQVRS 135
 DB 406 NPQNDTVILRFQVRS 420
 RESULT 14
 AAM41047
 ID AAM41047 standard; protein; 1016 AA.
 XX
 AC AAM41047;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 5978.
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 FN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-FSDB; AAI60203.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 as central nervous system injuries.
 XX
 PS Example 2; SEQ ID NO 5978; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 encoded polypeptides (AAM38642-AAM42213) with nootropic,
 immunosuppressant and cytostatic activity. The polynucleotides are useful
 in gene therapy. A composition containing a polypeptide or polynucleotide
 of the invention may be used to treat diseases of the peripheral nervous
 system, such as peripheral nervous injuries, peripheral neuropathy and
 localised neuropathies and central nervous system diseases, such as
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 utilisation of the activities such as: Immune system suppression,
 Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 assays for receptor activity, arthritis and inflammation, leukaemias and
 C.N.S disorders. Note: The sequence data for this patent did not form
 part of the printed specification

RESULT 13
 ABU03761
 ID ABU03761 standard; protein; 979 AA.
 XX
 AC ABU03761;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #427.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 FN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 427; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 979 AA;
 Query Match 100.0%; Score 135; DB 6; Length 979;
 Best Local Similarity 100.0%; Pred. No. 2.3e-132;
 Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLRLKVPYDNGVVRGYLSVFLE 60
 DB 286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLRLKVPYDNGVVRGYLSVFLE 345

```

XX SQ Sequence 1016 AA;
Query Match 100.0%; Score 135; DB 4; Length 1016;
Best Local Similarity 100.0%; Pred. No. 2.4e-132;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDNGVGRGYLSVPLE 60
Db 323 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDNGVGRGYLSVPLE 382

Qy 61 LSAGLPETSKYEXYRVMVHQSCNDPTKNIIREFASDFEVEGECWGYNRFRLDLLANEGYL 120
Db 383 LSAGLPETSKYEXYRVMVHQSCNDPTKNIIREFASDFEVEGECWGYNRFRLDLLANEGYL 442

Qy 121 NPQNDTVILRFQVRS 135
Db 443 NPQNDTVILRFQVRS 457

RESULT 15
ABU03764
ID ABU03764 standard; protein; 1016 AA.
AC ABU03764;
XX
XX 29-JAN-2003 (first entry)
DT Human expressed protein tag (EPT) #430.
DE
DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336378P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCO INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 430; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and

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CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1016 AA;
Query Match 100.0%; Score 135; DB 6; Length 1016;
Best Local Similarity 100.0%; Pred. No. 2.4e-132;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDNGVGRGYLSVPLE 60
Db 323 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDNGVGRGYLSVPLE 382

Qy 61 LSAGLPETSKYEXYRVMVHQSCNDPTKNIIREFASDFEVEGECWGYNRFRLDLLANEGYL 120
Db 383 LSAGLPETSKYEXYRVMVHQSCNDPTKNIIREFASDFEVEGECWGYNRFRLDLLANEGYL 442

Qy 121 NPQNDTVILRFQVRS 135
Db 443 NPQNDTVILRFQVRS 457

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Search completed: July 20, 2005, 20:47:42
Job time : 96.5357 secs

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:38:00 ; Search time 19.2857 Seconds
(without alignments)
673.517 Million cell updates/sec

Title: US-09-706-325-25
Perfect score: 135
Sequence: 1 ELVPSYDSATFVLENFSTLR.....NEGYLNPQNDTVILRFQVRS 135

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	5.9	210	2	A69898
2	7	5.2	253	2	T36718
3	7	5.2	257	2	C72418
4	7	5.2	285	2	H75032
5	7	5.2	316	2	T27194
6	7	5.2	377	2	AC3426
7	7	5.2	444	2	T35794
8	7	5.2	507	2	T48645
9	7	5.2	507	2	AD1336
10	7	5.2	507	2	AB1707
11	7	5.2	512	2	G69670
12	7	5.2	548	2	E89910
13	7	5.2	727	2	C84534
14	7	5.2	818	2	F96586
15	7	5.2	904	2	T04377
16	7	5.2	1777	2	T00490
17	6	4.4	38	2	F36491
18	6	4.4	77	2	G90411
19	6	4.4	80	2	A60699
20	6	4.4	86	2	T07829
21	6	4.4	89	2	D83372
22	6	4.4	98	2	T03585
23	6	4.4	101	2	T07828
24	6	4.4	102	2	F71354
25	6	4.4	112	2	C55993
26	6	4.4	115	2	T21833
27	6	4.4	120	2	P00026
28	6	4.4	124	2	C70537
29	6	4.4	127	2	A64927

hypothetical prote
hypothetical prote
transcription regu
conserved hypothet
transcription regu
probable membrane
3-hydroxybutyryl-C
extensin - carrot
hypothetical prote
hypothetical prote
cysteine dioxygena
hypothetical prote
hypothetical prote
type 4 fimbrial bi
pilus assembly pro
senescence-associat
senescence-associat
hypothetical prote
hypothetical prote
ttnR protein - Pee
resolvase - Escher
resolvase (EC 6.5.
fimbrial-like prot
probable fimbrial-
probable fimbrial-
hypothetical prote
hypothetical prote
probable signal se
protein-export pro
probable peptidyl-
maf protein (impor
probable peptidyl-
D83 protein (impor
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
DNA-directed RNA p
unknown protein en
hypothetical prote
NADH dehydrogenase
probable transcrip
probable transmem
oxidoreductase, sh
hypothetical prote
probable adenosylh
5-methylthioadenos
FixK-like regulato
conserved hypothet
hypothetical prote
hypothetical prote
sulfate ABC transp
hypothetical prote
phosphonates trans
hypothetical prote
heat shock protein
type III export pr
transcription regu
hypothetical prote
probable amino aci
hypothetical prote
iron(III) dicitrat
USF protein homolo
probable enoyl-CoA
hydroxyproline-ric
transcription fact
thua protein (impo
SAM-dependent meth
probable ARAC-type

103	6	4.4	274	2	B86024	probable ARAC-type	176	6	4.4	343	2	AF1783	polyol dehydrogena
104	6	4.4	274	2	S47736	probable transcrip	177	6	4.4	343	2	T19979	hypothetical prote
105	6	4.4	275	2	H86950	probable ABC-trans	178	6	4.4	344	2	H82656	twitching motility
106	6	4.4	277	2	A33595	probable transposo	179	6	4.4	344	2	JN0055	twitching motility
107	6	4.4	278	2	S20790	extensin - almond	180	6	4.4	345	2	S55969	H+-exporting ATPas
108	6	4.4	278	2	H96639	protein Tif9.4 (im	181	6	4.4	346	1	JH0387	alkanal monooxygen
109	6	4.4	279	2	E69595	transcription acti	182	6	4.4	346	2	D90244	hypothetical prote
110	6	4.4	283	2	C87346	hypothetical prote	183	6	4.4	346	2	G75486	probable type I to
111	6	4.4	285	2	H90488	arabinose ABC tran	184	6	4.4	350	2	T14191	extensin homolog 1
112	6	4.4	286	2	B70833	carbon-monoxide de	185	6	4.4	350	2	T25366	hypothetical prote
113	6	4.4	286	2	A84063	hypothetical prote	186	6	4.4	350	2	H86371	40.0K hypothetical
114	6	4.4	287	2	G86707	divalent cation tr	187	6	4.4	351	2	T01845	hypothetical prote
115	6	4.4	288	2	T22721	hypothetical prote	188	6	4.4	352	2	T10905	adenylate cyclase
116	6	4.4	289	2	A12179	hypothetical prote	189	6	4.4	352	2	JC5382	hereditary hemochr
117	6	4.4	291	1	NCBP75	phosphodiesterase	190	6	4.4	359	2	S68471	asparaginase (EC 3
118	6	4.4	291	2	D64377	ribosomal protein	191	6	4.4	362	2	C90674	hypothetical prote
119	6	4.4	292	2	H96784	hypothetical prote	192	6	4.4	362	2	T50582	FecCD-family membr
120	6	4.4	296	1	NMECMG	maltose transport	193	6	4.4	365	2	F85524	hypothetical prote
121	6	4.4	296	2	AB1014	maltose transport	194	6	4.4	368	2	G83015	3-dehydroquinatase
122	6	4.4	296	2	S05333	maltose transport	195	6	4.4	369	2	F83250	histidinol-phospha
123	6	4.4	296	2	C86096	part of maltose pe	196	6	4.4	370	2	S27344	hupK protein - Rhi
124	6	4.4	296	2	G91255	transport system p	197	6	4.4	370	2	A83621	probable ATP-bindi
125	6	4.4	296	2	A60175	maltose transport	198	6	4.4	372	2	B41874	heat shock protein
126	6	4.4	296	2	AD0452	maltose transport	199	6	4.4	372	2	AD2111	twitching motility
127	6	4.4	297	2	F87567	integral membrane	200	6	4.4	376	2	D72493	hypothetical prote
128	6	4.4	297	2	C83143	hypothetical prote	201	6	4.4	378	2	S25279	flagellar motor sw
129	6	4.4	299	2	S12022	extensin - rape	202	6	4.4	380	2	H81152	antidion nuclease
130	6	4.4	300	2	A70616	probable ephr prot	203	6	4.4	381	2	B84935	acetylornithine de
131	6	4.4	301	2	C69143	hypothetical prote	204	6	4.4	386	2	T12845	hypothetical prote
132	6	4.4	301	2	T52437	PRM1 homolog (lipo	205	6	4.4	388	2	T32153	hypothetical prote
133	6	4.4	305	2	JC4920	2-oxoacid-faradox	206	6	4.4	390	2	T16782	hypothetical prote
134	6	4.4	305	2	B81426	methionyl-tRNA for	207	6	4.4	394	2	E83903	thiolase (acetyl-C
135	6	4.4	305	2	T34309	hypothetical prote	208	6	4.4	399	2	D86322	hypothetical prote
136	6	4.4	306	2	A24354	extensin precursor	209	6	4.4	400	2	T32705	hypothetical prote
137	6	4.4	307	2	S54080	carrier protein YM	210	6	4.4	405	2	C90194	hypothetical prote
138	6	4.4	308	2	H65035	hypothetical prote	211	6	4.4	411	2	D72588	hypothetical prote
139	6	4.4	308	2	C91059	probable transcrip	212	6	4.4	412	2	T30079	hypothetical prote
140	6	4.4	308	2	A85904	probable transcrip	213	6	4.4	412	2	JC1116	type III site-spec
141	6	4.4	310	2	T44857	probable hydroxylo	214	6	4.4	413	2	T26403	hypothetical prote
142	6	4.4	310	2	S12807	cnjC protein, conj	215	6	4.4	421	2	E96522	hypothetical prote
143	6	4.4	311	2	T32915	hypothetical prote	216	6	4.4	432	2	T35527	hypothetical prote
144	6	4.4	312	2	B69170	UDP-N-acetylmuram	217	6	4.4	433	2	D87636	amino acid permeas
145	6	4.4	312	2	AB1233	hypothetical prote	218	6	4.4	433	2	AH2369	sulfide-quinone re
146	6	4.4	313	2	D83961	malonyl CoA-acyl c	219	6	4.4	434	2	D86530	N utilization prot
147	6	4.4	313	2	G71886	hypothetical prote	220	6	4.4	434	2	E72093	N utilization subs
148	6	4.4	313	2	D64626	hypothetical prote	221	6	4.4	434	2	H81709	N utilization subs
149	6	4.4	313	2	AD1352	S. aureus Cbf1 pro	222	6	4.4	434	2	A71559	probable transcrip
150	6	4.4	315	2	B96533	hypothetical prote	223	6	4.4	438	1	S11225	transcription fact
151	6	4.4	316	2	F81330	hypothetical prote	224	6	4.4	438	2	S77655	hypothetical prote
152	6	4.4	316	2	T52464	hypothetical prote	225	6	4.4	439	2	E75118	probable threonine
153	6	4.4	316	2	B71082	hypothetical prote	226	6	4.4	440	1	A35875	transcription fact
154	6	4.4	318	2	H81255	hypothetical prote	227	6	4.4	440	1	A35875	transcription fact
155	6	4.4	318	2	G82350	lipid A biosynthes	228	6	4.4	440	2	AE1395	conserved hypothet
156	6	4.4	320	2	F70034	conserved hypothet	229	6	4.4	440	2	AH1770	conserved hypothet
157	6	4.4	320	2	D97197	hypothetical prote	230	6	4.4	440	2	H71013	probable threonine
158	6	4.4	326	2	S36705	duRP diphosphatase	231	6	4.4	441	1	A53988	transcription fact
159	6	4.4	326	2	T42552	duRP diphosphatase	232	6	4.4	441	1	TVCHTE	transcription fact
160	6	4.4	326	2	S32585	structural pro-ein	233	6	4.4	441	1	TVHUET	transcription fact
161	6	4.4	326	2	D95309	probable UDP-gluc	234	6	4.4	443	2	A99657	hypothetical prote
162	6	4.4	327	2	AH3216	UDP-glucose 4-epim	235	6	4.4	443	2	A85508	hypothetical prote
163	6	4.4	328	2	B59296	alpha-N-arabinofur	236	6	4.4	444	2	E83033	probable MFS trans
164	6	4.4	329	2	T24701	hypothetical prote	237	6	4.4	444	2	AH3613	hypothetical prote
165	6	4.4	329	2	C96033	probable regulator	238	6	4.4	446	2	G75304	conserved hypothet
166	6	4.4	330	2	S22140	nodulin Enod2 - Se	239	6	4.4	448	1	H69032	polyferredoxin 2 -
167	6	4.4	331	2	A71338	conserved hypothet	240	6	4.4	450	2	H81338	probable sugar tra
168	6	4.4	331	2	E86621	aspartate dehydrog	241	6	4.4	452	2	A82777	anthranilate synth
169	6	4.4	333	2	G72002	aspartate dehydrog	242	6	4.4	454	2	S75610	UDP-N-acetylmuram
170	6	4.4	333	2	T01846	hypothetical prote	243	6	4.4	458	2	A83391	probable glutamine
171	6	4.4	335	2	B75091	pyruvate formate-l	244	6	4.4	458	2	H83609	probable glutamine
172	6	4.4	337	1	B71052	hypothetical prote	245	6	4.4	458	2	C86860	hypothetical prote
173	6	4.4	341	2	G86315	hypothetical prote	246	6	4.4	458	2	C97151	hypothetical prote
174	6	4.4	342	2	AC3274	hydroxymethylbilan	247	6	4.4	461	2	G75598	acetyl-CoA acetyl
175	6	4.4	343	2	AF1407	polyol dehydrogena	248	6	4.4	462	1	JC4686	juvenile-hormone e

249	6	4.4	463	2	D88104	protein W10G11.19	322	6	4.4	564	2	S06896	nucleocapsid prote
250	6	4.4	466	2	AF2274	hypothetical prote	323	6	4.4	568	2	S28089	hypothetical prote
251	6	4.4	468	2	B87158	PPF-family protein	324	6	4.4	570	2	C97408	long-chain-fatty-a
252	6	4.4	470	1	S56565	hypothetical 53K p	325	6	4.4	570	2	AD2626	long-chain-fatty-a
253	6	4.4	470	2	F31291	probable regulator	326	6	4.4	572	2	S64387	protein kinase DBF
254	6	4.4	470	2	H86132	probable regulator	327	6	4.4	573	2	B70726	probable secd - My
255	6	4.4	472	1	A53236	transcription fact	328	6	4.4	573	2	B70942	hypothetical prote
256	6	4.4	473	2	JH0754	sucrose-6-phosphat	329	6	4.4	576	2	T48573	hypothetical prote
257	6	4.4	473	2	D88976	protein P54E2.4 [i	330	6	4.4	581	2	A97119	probable membrane
258	6	4.4	475	2	T24900	hypothetical prote	331	6	4.4	581	2	C84749	hypothetical prote
259	6	4.4	477	2	AG0905	RNA polymerase sig	332	6	4.4	586	1	S34731	amylase [EC 3.2.1.
260	6	4.4	477	2	A35695	transcription init	333	6	4.4	587	2	AG3019	conserved hypothet
261	6	4.4	477	2	D85984	RNA polymerase sig	334	6	4.4	592	2	T21536	hypothetical prote
262	6	4.4	477	2	A88139	RNA polymerase sig	335	6	4.4	602	2	D75618	hypothetical prote
263	6	4.4	477	2	A24115	transcription init	336	6	4.4	602	2	E90568	DNA primase [impor
264	6	4.4	477	2	A11026	regulatory protein	337	6	4.4	603	2	S06059	gene ND1 intron 4
265	6	4.4	477	2	S62824	preprotein translo	338	6	4.4	605	2	T39837	dnak-type molecula
266	6	4.4	480	2	G70678	hypothetical prote	339	6	4.4	607	2	T20796	hypothetical prote
267	6	4.4	481	2	S11979	threonine synthase	340	6	4.4	614	2	T20795	hypothetical prote
268	6	4.4	481	2	A89102	protein P25E5.4 [i	341	6	4.4	615	2	F64572	arginine decarboxy
269	6	4.4	481	2	B70908	hypothetical prote	342	6	4.4	615	2	C71867	arginine decarboxy
270	6	4.4	485	1	TVCHET	transcription fact	343	6	4.4	618	2	B64564	transketolase B -
271	6	4.4	486	2	AF1575	acetaldehyde dehyd	344	6	4.4	618	2	H71946	1-deoxyxylulose-5-
272	6	4.4	486	2	AC1222	acetaldehyde dehyd	345	6	4.4	620	2	S06733	hydroxyproline-xic
273	6	4.4	487	2	T21645	hypothetical prote	346	6	4.4	628	2	AB0548	PrpE protein [impo
274	6	4.4	488	1	TVFVES	transcription fact	347	6	4.4	634	2	B98265	hypothetical prote
275	6	4.4	491	1	JN0491	X-Pro aminopeptida	348	6	4.4	638	2	A82260	penicillin-binding
276	6	4.4	491	1	CEECAM	UDP-N-acetylmuram	349	6	4.4	638	2	AH0340	putative autotransp
277	6	4.4	491	2	AF0518	UDP-N-acetyl-muram	350	6	4.4	645	2	H70173	probable long-chai
278	6	4.4	491	2	G85491	UDP-N-acetyl-muram	351	6	4.4	646	2	T47154	hypothetical prote
279	6	4.4	491	2	G90640	UDP-N-acetyl-muram	352	6	4.4	646	2	G84854	hypothetical prote
280	6	4.4	491	2	A10068	UDP-N-acetyl-muram	353	6	4.4	647	2	B34457	204 protein - mous
281	6	4.4	491	2	B96633	hypothetical prote	354	6	4.4	654	2	B84017	hypothetical prote
282	6	4.4	492	2	T43346	nuclear receptor N	355	6	4.4	657	2	B84869	probable Sfl6 prot
283	6	4.4	494	2	H75587	conserved hypothet	356	6	4.4	672	2	G87386	TPR domain protein
284	6	4.4	496	2	C87194	probable transmemb	357	6	4.4	680	2	JC5133	protein-glutamine
285	6	4.4	497	1	S31337	glucose-6-phosphat	358	6	4.4	684	2	T48357	hypothetical prote
286	6	4.4	498	1	D71179	probable sugar ABC	359	6	4.4	687	2	D84126	penicillin-binding
287	6	4.4	498	2	E72493	probable ribose AB	360	6	4.4	692	2	AD1857	hypothetical prote
288	6	4.4	498	2	H75161	ribose abc transpo	361	6	4.4	694	2	T01005	hypothetical prote
289	6	4.4	499	2	H70453	virulence factor M	362	6	4.4	695	2	T52429	PRM1 homolog [impo
290	6	4.4	500	2	S16788	probable reverse t	363	6	4.4	696	2	G71829	probable outer mem
291	6	4.4	508	2	A72201	UDP-sugar diphosph	364	6	4.4	699	1	XEBYUG	UDPglucose 4-epime
292	6	4.4	514	1	B31997	IMP dehydrogenase	365	6	4.4	699	2	T05225	extensin homolog F
293	6	4.4	514	1	A31997	IMP dehydrogenase	366	6	4.4	706	2	G82943	hypothetical UU029
294	6	4.4	514	1	J70565	IMP dehydrogenase	367	6	4.4	713	2	T40051	hypothetical prote
295	6	4.4	518	2	A12426	hypothetical prote	368	6	4.4	721	2	T40317	actin-like protein
296	6	4.4	519	2	B87233	probable secreted	369	6	4.4	722	2	E71403	hypothetical prote
297	6	4.4	520	2	T14752	microphthalmia-ass	370	6	4.4	726	2	S62180	nuclear pore prote
298	6	4.4	523	1	S30805	probable RNA helic	371	6	4.4	732	1	S23864	translation elonga
299	6	4.4	523	2	D93631	probable sulfate t	372	6	4.4	735	2	S57486	ferrihydrogobactin
300	6	4.4	525	2	A96183	D-ribulokinase [EC	373	6	4.4	735	2	T50068	probable ATP-depen
301	6	4.4	525	2	A31303	ribitol kinase [im	374	6	4.4	743	2	E71432	hypothetical prote
302	6	4.4	528	2	G90569	hypothetical prote	375	6	4.4	752	2	G85941	hypothetical prote
303	6	4.4	529	1	M2EC8	58K mobilization p	376	6	4.4	752	2	C91096	hypothetical prote
304	6	4.4	529	2	S51477	extracellular glyc	377	6	4.4	752	2	B65070	probable oxidoredu
305	6	4.4	530	2	A18335	methionyl-tRNA syn	378	6	4.4	753	2	A96747	probable RNA-bindi
306	6	4.4	535	2	C83395	probable acyl-CoA	379	6	4.4	756	2	S74742	exopolysaccharide
307	6	4.4	536	2	T04234	calmodulin-binding	380	6	4.4	760	2	T06291	extensin homolog T
308	6	4.4	540	2	JC4916	signal transducing	381	6	4.4	773	2	T44989	transducer protein
309	6	4.4	541	2	T33583	hypothetical prote	382	6	4.4	776	2	S45495	isp4 protein - fis
310	6	4.4	543	1	ERADDG	fiber protein - ca	383	6	4.4	789	2	S46631	aconitate hydratase
311	6	4.4	544	2	T13877	NAHD2 dehydrogenas	384	6	4.4	807	2	F85647	probable outer mem
312	6	4.4	544	2	S54531	hypothetical prote	385	6	4.4	807	2	F64844	ydcS protein precu
313	6	4.4	550	2	S25202	spiramycin-resista	386	6	4.4	807	2	F90787	probable outer mem
314	6	4.4	551	2	B64005	hypothetical prote	387	6	4.4	811	2	E97040	phage related prot
315	6	4.4	551	2	D83277	electron transfer	388	6	4.4	822	2	T41941	glycoprotein B - h
316	6	4.4	552	2	T28752	phenylalanine-tRNA	389	6	4.4	830	2	T36683	probable integral
317	6	4.4	552	2	S48328	hypothetical prote	390	6	4.4	832	2	S19418	probable membrane
318	6	4.4	560	2	T08750	hypothetical prote	391	6	4.4	837	2	H84239	dimethylsulfoxide
319	6	4.4	564	1	VHXPUV	major structural n	392	6	4.4	842	2	S18462	glycoprotein H pre
320	6	4.4	564	1	VHXPMV	major structural n	393	6	4.4	847	2	F96531	hypothetical prote
321	6	4.4	564	2	S12480	nucleocapsid prote	394	6	4.4	876	2	G90592	hypothetical prote

395	6	4.4	886	2	S48371	hypothetical prote	468	6	4.4	2475	2	T00047	gellan lyase (EC 4
396	6	4.4	887	2	S57430	probable format d	469	6	4.4	2489	2	S59782	probable membrane
397	6	4.4	892	2	T27005	hypothetical prote	470	6	4.4	2809	2	T30213	G-cadherin - sea u
398	6	4.4	895	2	T32374	hypothetical prote	471	6	4.4	3083	2	AH2493	hypothetical prote
399	6	4.4	899	2	H96617	probable disease r	472	6	4.4	3535	2	E83641	probable hemagglut
400	6	4.4	899	2	B48586	suppressor of hair	473	6	4.4	3746	1	YGPLV3	alpha-aminoadipyl-
401	6	4.4	900	2	G96617	probable disease r	474	6	4.4	3791	1	YGPLV8	alpha-aminoadipyl-
402	6	4.4	900	2	S86264	55.11 protein homo	475	6	4.4	5627	2	C83339	hypothetical prote
403	6	4.4	906	2	AD3267	protein translocas	476	6	4.4	6658	2	T13931	projectin - fruit
404	6	4.4	913	2	E75554	valyl-tRNA synthet	477	5	3.7	14	1	LFEBWC	trp operon leader
405	6	4.4	946	2	S28061	SCP1 protein - rat	478	5	3.7	17	2	A27486	folitropin inhibi
406	6	4.4	947	2	I49635	mouse Dhml protein	479	5	3.7	21	2	FC1310	small granule S3 c
407	6	4.4	956	2	G70327	isoleucine-tRNA li	480	5	3.7	33	2	H82078	hypothetical prote
408	6	4.4	958	2	C86308	F20D23.9 protein -	481	5	3.7	34	2	C44336	neurotoxin Tx3-3 -
409	6	4.4	967	2	S68852	hypothetical prote	482	5	3.7	35	2	JQ2193	hypothetical 3.9K
410	6	4.4	1012	2	B97326	endoglucanase fami	483	5	3.7	36	2	A37172	collagen alpha 1(X
411	6	4.4	1020	2	B82427	sensor protein Tor	484	5	3.7	37	2	A82057	ribosomal protein
412	6	4.4	1024	2	S71804	receptor-like serp	485	5	3.7	38	2	AG0028	50S ribosomal prot
413	6	4.4	1024	2	A83557	acriflavin resista	486	5	3.7	43	2	T33020	hypothetical prote
414	6	4.4	1035	1	A43090	enteropeptidase (E	487	5	3.7	44	2	T18729	hypothetical prote
415	6	4.4	1036	2	D70117	acriflavin resist	488	5	3.7	44	2	B46078	POU protein Emb, f
416	6	4.4	1046	2	F71432	hypothetical prote	489	5	3.7	45	2	B83689	hypothetical prote
417	6	4.4	1048	2	S64758	hypothetical prote	490	5	3.7	46	2	C82345	hypothetical prote
418	6	4.4	1048	2	T31653	hypothetical prote	491	5	3.7	46	2	A71571	hypothetical prote
419	6	4.4	1087	2	C84263	transmembrane olig	492	5	3.7	49	2	S11814	opacity protein (c
420	6	4.4	1095	2	I49270	Na+/K+/Cl-cotransp	493	5	3.7	51	2	F90802	hypothetical prote
421	6	4.4	1095	2	A54145	sodium-potassium-c	494	5	3.7	51	2	E85662	hypothetical prote
422	6	4.4	1099	2	I46498	bumetanide-sensiti	495	5	3.7	52	2	I40664	hook protein - Cau
423	6	4.4	1108	2	AF1047	probable membrane	496	5	3.7	53	2	S77936	exoskeletal protei
424	6	4.4	1112	2	H95964	probable outer mem	497	5	3.7	53	2	AF1734	hypothetical prote
425	6	4.4	1117	2	T19727	hypothetical prote	498	5	3.7	54	2	H82450	hypothetical prote
426	6	4.4	1127	2	S97580	hypothetical prote	499	5	3.7	56	1	ERBF1B	gene lB protein -
427	6	4.4	1131	2	T15787	hypothetical prote	500	5	3.7	56	2	AB1818	hypothetical prote
428	6	4.4	1170	2	S52525	probable membrane	501	5	3.7	57	2	JC5008	hypothetical prote
429	6	4.4	1189	2	T30319	Lian-Aal retrotran	502	5	3.7	57	2	D84196	protein translocas
430	6	4.4	1191	2	S76414	beta transducin-li	503	5	3.7	57	2	G97910	hypothetical prote
431	6	4.4	1202	2	T37867	hypothetical prote	504	5	3.7	57	2	AH0423	probable membrane
432	6	4.4	1204	2	C75015	probable pyrolysin	505	5	3.7	59	2	T07299	NADH dehydrogenase
433	6	4.4	1213	2	T41378	probable helicase	506	5	3.7	59	2	A69520	hypothetical prote
434	6	4.4	1225	2	A56514	chromokinesin - ch	507	5	3.7	60	2	E35156	thioredoxin-disulf
435	6	4.4	1236	2	E70977	hypothetical prote	508	5	3.7	60	2	D84173	hypothetical prote
436	6	4.4	1236	2	T19492	hypothetical prote	509	5	3.7	62	2	C90761	probable division
437	6	4.4	1250	2	S14177	SCD25 protein (ver	510	5	3.7	62	2	H85624	hypothetical prote
438	6	4.4	1286	1	S38058	hypothetical prote	511	5	3.7	62	2	S73032	hypothetical prote
439	6	4.4	1297	2	T39287	hypothetical prote	512	5	3.7	62	2	T14430	chromomethylase CM
440	6	4.4	1322	2	T24140	hypothetical prote	513	5	3.7	64	2	G97027	hypothetical prote
441	6	4.4	1328	2	T23007	hypothetical prote	514	5	3.7	65	2	C86210	protein P22G5.4 [i
442	6	4.4	1353	2	T00249	ich1 protein - ink	515	5	3.7	65	2	F83727	hypothetical prote
443	6	4.4	1378	2	T47605	RING finger-like p	516	5	3.7	66	2	S47027	DNA-directed RNA p
444	6	4.4	1382	2	T01789	protoporphyrin IX	517	5	3.7	67	2	G81110	hypothetical prote
445	6	4.4	1383	2	T07126	magnesium chelatas	518	5	3.7	68	1	JN0537	head protein gp3 -
446	6	4.4	1408	2	T43261	multidrug resistan	519	5	3.7	68	2	F90970	probable head comp
447	6	4.4	1431	2	A45866	dextranucrase (EC	520	5	3.7	68	2	JC4271	hypothetical 7.5k
448	6	4.4	1541	2	T30227	pipecolate-incorpo	521	5	3.7	69	2	E69169	hypothetical prote
449	6	4.4	1582	2	A56248	sulfonylurea recep	522	5	3.7	70	2	T14901	chlorismate mutase
450	6	4.4	1616	2	E90704	Rns core protein w	523	5	3.7	70	2	F72280	conserved hypotnet
451	6	4.4	1645	2	H85554	hypothetical prote	524	5	3.7	70	2	S76907	hypothetical prote
452	6	4.4	1651	2	F88750	protein vit-6 [imp	525	5	3.7	72	2	AE1038	hypothetical prote
453	6	4.4	1651	2	B43081	vitellogenin vit-6	526	5	3.7	72	2	T17937	hypothetical prote
454	6	4.4	1660	2	T18561	vitellogenin vit-6	527	5	3.7	72	2	B81034	hypothetical prote
455	6	4.4	1694	2	A83512	hypothetical prote	528	5	3.7	72	2	C75519	hypothetical prote
456	6	4.4	1742	2	S24600	projectin - fruit	529	5	3.7	72	2	T11975	hypothetical prote
457	6	4.4	1747	2	T43162	vitellogenin - gyp	530	5	3.7	72	2	T25597	hypothetical prote
458	6	4.4	1767	2	H97912	conserved hypotnet	531	5	3.7	73	2	G87164	hypothetical prote
459	6	4.4	1784	2	C96615	hypothetical prote	532	5	3.7	74	2	S13515	retinoic acid rece
460	6	4.4	1807	2	JC6319	integrin beta-4 ch	533	5	3.7	75	2	F75031	hydrogenase expres
461	6	4.4	1871	2	D96698	probable DNA polym	534	5	3.7	75	2	F75345	hypothetical prote
462	6	4.4	1894	2	T02155	DNA-directed DNA p	535	5	3.7	75	2	F97837	proline/betaine tr
463	6	4.4	2078	2	T25400	hypothetical prote	536	5	3.7	75	2	AE1588	hypothetical prote
464	6	4.4	2163	2	T15276	hypothetical prote	537	5	3.7	75	2	AF1651	hypothetical prote
465	6	4.4	2201	2	A54774	ATP binding casset	538	5	3.7	76	2	H81214	hypothetical prote
466	6	4.4	2271	2	F90073	hypothetical prote	539	5	3.7	76	2	S72752	B1496 Cl 130 prote
467	6	4.4	2298	2	T49648	hypothetical prote	540	5	3.7	76	2	T24627	hypothetical prote

541	5	3.7	76	2	G82544	hypothetical prote	614	5	3.7	105	2	T31300	hypothetical prote
542	5	3.7	77	2	S36032	hemadin precursor	615	5	3.7	105	2	T14666	hypothetical prote
543	5	3.7	77	2	A05190	hypothetical prote	616	5	3.7	105	2	AD2633	hypothetical prote
544	5	3.7	77	2	G36769	17R protein - huma	617	5	3.7	106	2	S69868	hypothetical prote
545	5	3.7	80	2	A01906	hypothetical prote	618	5	3.7	106	2	D72476	hypothetical prote
546	5	3.7	80	2	C82761	hypothetical prote	619	5	3.7	106	2	E97727	hypothetical prote
547	5	3.7	82	2	D4562	hypothetical prote	620	5	3.7	106	2	C81988	hypothetical prote
548	5	3.7	82	2	T18159	hypothetical prote	621	5	3.7	106	2	JQ0234	hypothetical 12.5K
549	5	3.7	82	2	T10869	y4KO protein - Rhi	622	5	3.7	107	1	SSUL	stellacyanin - Jap
550	5	3.7	83	2	A82906	hypothetical prote	623	5	3.7	107	2	AB1051	hypothetical prote
551	5	3.7	83	2	T07252	hypothetical prote	624	5	3.7	107	2	S53575	probable membrane
552	5	3.7	83	2	D84697	hypothetical prote	625	5	3.7	107	2	A44355	Cu44 glycoprotein
553	5	3.7	83	2	T18171	hypothetical prote	626	5	3.7	107	2	B31915	hypothetical prote
554	5	3.7	85	2	G59207	thioredoxin - Meth	627	5	3.7	108	2	AD2458	hypothetical prote
555	5	3.7	85	2	H84728	hypothetical prote	628	5	3.7	108	1	D71209	ribosomal protein
556	5	3.7	85	2	T18143	hypothetical prote	629	5	3.7	109	2	JC2440	biphenyl dioxygena
557	5	3.7	85	2	F96949	hypothetical prote	630	5	3.7	109	2	C31183	photosystem II pro
558	5	3.7	86	2	D33989	Ig heavy chain V-4	631	5	3.7	109	2	S69581	hypothetical prote
559	5	3.7	86	2	T31846	hypothetical prote	632	5	3.7	109	2	A72546	hypothetical prote
560	5	3.7	86	2	A10179	hypothetical prote	633	5	3.7	109	2	G81244	pHnA protein NMB00
561	5	3.7	87	2	S41306	hypothetical prote	634	5	3.7	109	2	F82023	pHnA protein homol
562	5	3.7	87	2	S44877	ZC21.5 protein - C	635	5	3.7	109	2	B70037	hypothetical prote
563	5	3.7	89	2	T43992	hypothetical prote	636	5	3.7	109	2	T29794	hypothetical prote
564	5	3.7	89	2	A64651	conserved hypotet	637	5	3.7	109	2	C84386	hypothetical prote
565	5	3.7	89	2	D71940	hypothetical prote	638	5	3.7	110	2	AE2282	mutator MutT prote
566	5	3.7	89	2	AG3394	hypothetical membr	639	5	3.7	110	2	C64598	hypothetical prote
567	5	3.7	90	2	JR0210	proteinase (BC 3.4	640	5	3.7	111	1	JC7085	ferredoxin [2Fe-2S
568	5	3.7	91	2	S25462	Ig kappa chain V r	641	5	3.7	111	2	B75084	hypothetical prote
569	5	3.7	92	1	RHSER	ribosomal protein	642	5	3.7	111	2	T36555	probable membrane
570	5	3.7	92	2	A30574	macrophage inflam	643	5	3.7	111	2	B84046	hypothetical prote
571	5	3.7	92	2	I54781	fibroblast growth	644	5	3.7	111	2	AF0139	probable starvatio
572	5	3.7	92	2	A86197	protein F9P14.1 [i	645	5	3.7	111	2	S48974	hypothetical prote
573	5	3.7	92	2	C69454	hypothetical prote	646	5	3.7	111	2	JC2020	peptide transporte
574	5	3.7	93	2	B35673	LD78-beta protein	647	5	3.7	112	2	B24773	protein-tyrosine k
575	5	3.7	94	1	F75022	ribosomal protein	648	5	3.7	112	2	AE0451	hypothetical prote
576	5	3.7	94	2	S10732	hypothetical prote	649	5	3.7	113	1	Q0ECXQ	hypothetical prote
577	5	3.7	94	2	G86658	hypothetical prote	650	5	3.7	113	2	C24773	protein-tyrosine k
578	5	3.7	94	2	H75341	hypothetical prote	651	5	3.7	113	2	S16254	hypothetical prote
579	5	3.7	94	2	C97048	hypothetical prote	652	5	3.7	113	2	AD1039	hypothetical prote
580	5	3.7	95	1	WSWLSB	E5B protein - bovi	653	5	3.7	113	2	AB1646	hypothetical prote
581	5	3.7	95	2	A56644	inverted repeat co	654	5	3.7	113	2	T35806	hypothetical prote
582	5	3.7	95	2	F83887	hypothetical prote	655	5	3.7	114	2	F83959	ribosomal protein
583	5	3.7	95	2	S84537	probable membrane	656	5	3.7	114	2	JC5482	hypothetical 13.2K
584	5	3.7	95	2	E81360	probable periplasm	657	5	3.7	114	2	F90557	hypothetical prote
585	5	3.7	96	2	S49377	translation releas	658	5	3.7	114	2	B84710	hypothetical prote
586	5	3.7	96	2	A46066	hypothetical prote	659	5	3.7	114	2	S77061	transposase sil066
587	5	3.7	96	2	S89798	holin protein, 10.	660	5	3.7	115	2	B83407	hypothetical prote
588	5	3.7	97	1	A47365	defensin alpha-4 p	661	5	3.7	115	2	AH1891	hypothetical prote
589	5	3.7	98	2	S68136	NADH2 dehydrogenas	662	5	3.7	116	1	THUAP	glycoprotein hormo
590	5	3.7	98	2	B64360	hypothetical prote	663	5	3.7	116	2	S76118	hypothetical prote
591	5	3.7	99	1	QQQYBW	hypothetical prote	664	5	3.7	116	2	AI2039	hypothetical prote
592	5	3.7	99	2	D30484	hypothetical prote	665	5	3.7	116	2	B64451	hypothetical prote
593	5	3.7	99	2	T39208	very hypothetical	666	5	3.7	117	2	T47990	hypothetical prote
594	5	3.7	99	2	T01678	hypothetical prote	667	5	3.7	117	2	AB2757	hypothetical prote
595	5	3.7	100	2	E96121	cytochrome b (562)	668	5	3.7	118	2	CH2967	6-pyruvoyltetrahyd
596	5	3.7	100	2	S86121	hypothetical prote	669	5	3.7	118	2	C98315	exsC protein (AJ22
597	5	3.7	100	2	S37793	hypothetical prote	670	5	3.7	118	2	S49946	probable membrane
598	5	3.7	100	2	S89744	hypothetical prote	671	5	3.7	118	2	T35739	probable integral
599	5	3.7	100	2	A82479	hypothetical prote	672	5	3.7	118	2	T17380	vIAA protein - Dic
600	5	3.7	101	2	S69300	hypothetical prote	673	5	3.7	118	2	AF2022	hypothetical prote
601	5	3.7	101	2	A88500	protein K04G7.12 [674	5	3.7	118	2	AG1004	conserved hypotet
602	5	3.7	101	2	D83375	hypothetical prote	675	5	3.7	118	2	B64630	hypothetical prote
603	5	3.7	101	2	H81352	small hydrophobic	676	5	3.7	118	2	T27456	hypothetical prote
604	5	3.7	102	2	A11153	PTS system, fructo	677	5	3.7	119	2	H83744	hypothetical prote
605	5	3.7	102	2	A75417	hypothetical prote	678	5	3.7	119	2	AC1161	Chemotaxis respons
606	5	3.7	102	2	H70973	hypothetical prote	679	5	3.7	119	2	AC1520	Chemotaxis respons
607	5	3.7	103	2	D82165	hypothetical prote	680	5	3.7	119	2	F81735	conserved hypotet
608	5	3.7	104	1	BVECAA	artA protein - Bsc	681	5	3.7	119	2	D71473	probable iojap - C
609	5	3.7	104	2	S04719	ribosomal protein	682	5	3.7	119	2	G85998	hypothetical prote
610	5	3.7	104	2	T13549	hypothetical prote	683	5	3.7	119	2	C65128	hypothetical prote
611	5	3.7	104	2	B69058	hypothetical prote	684	5	3.7	119	2	C91153	hypothetical prote
612	5	3.7	104	2	H69261	hypothetical prote	685	5	3.7	119	2	AF3411	phosphohydrolase (
613	5	3.7	105	2	H87543	conserved hypotet	686	5	3.7	120	1	UTPGA	glycoprotein hormo

687	5	3.7	120	2	C91027	D-erythro-7,8-dihy	760	5	3.7	130	2	AH2381	glycine cleavage s
688	5	3.7	120	2	B65002	D-erythro-7,8-dihy	761	5	3.7	130	2	AH1125	hypothetical prote
689	5	3.7	120	2	D85871	D-erythro-7,8-dihy	762	5	3.7	130	2	AG1486	hypothetical prote
690	5	3.7	120	2	I51241	pituitary glycopro	763	5	3.7	131	1	SIPSDP	steroid Delta-iso
691	5	3.7	120	2	A45585	glycoprotein hormo	764	5	3.7	131	2	H82337	preprotein translo
692	5	3.7	120	2	G00021	chlorionic gonadotr	765	5	3.7	131	2	S65197	probable membrane
693	5	3.7	120	2	A39555	glycoprotein hormo	766	5	3.7	131	2	T01487	hypothetical prote
694	5	3.7	120	2	S53062	glycoprotein hormo	767	5	3.7	132	1	JVB9PL	DNA-packaging prot
695	5	3.7	120	2	C29585	homeotic protein H	768	5	3.7	132	2	E90900	probable DNA-packa
696	5	3.7	120	2	T17514	hypothetical prote	769	5	3.7	132	2	D90833	DNA packaging prot
697	5	3.7	120	2	A87594	bleomycin resistan	770	5	3.7	132	2	AE0224	flagellar protein
698	5	3.7	120	2	AF0299	probable membrane	771	5	3.7	132	2	S04830	regulatory protein
699	5	3.7	120	2	A13137	hypothetical prote	772	5	3.7	132	2	G72774	hypothetical prote
700	5	3.7	120	2	D90546	proline dipeptidas	773	5	3.7	132	2	D87574	unknown protein, 4
701	5	3.7	121	2	B70187	ribosomal protein	774	5	3.7	132	2	H86416	probable auxin-ind
702	5	3.7	121	2	S06615	chorion protein s1	775	5	3.7	132	2	C86417	hypothetical prote
703	5	3.7	121	2	D97840	hypothetical prote	776	5	3.7	132	2	I40566	hypothetical prote
704	5	3.7	121	2	YLHUA	serum amyloid A2 p	777	5	3.7	133	2	T04081	probable ribosomal
705	5	3.7	122	1	YLHUS	serum amyloid A1 p	778	5	3.7	133	2	A44870	fatty acid-binding
706	5	3.7	122	2	D41287	Ig heavy chain V-I	779	5	3.7	133	2	C85583	probable tail comp
707	5	3.7	122	2	I39456	serum amyloid A2-b	780	5	3.7	133	2	A90733	probable minor tai
708	5	3.7	122	2	B72637	hypothetical prote	781	5	3.7	133	2	B84101	flagellar protein
709	5	3.7	122	2	E72584	hypothetical prote	782	5	3.7	133	2	T23921	hypothetical prote
710	5	3.7	122	2	T17850	hypothetical prote	783	5	3.7	133	2	JC2007	differentiation in
711	5	3.7	122	2	T40756	hypothetical prote	784	5	3.7	133	2	B86754	prophage pi2 prote
712	5	3.7	122	2	B90760	hypothetical prote	785	5	3.7	133	2	A86418	probable auxin-ind
713	5	3.7	122	2	E84837	hypothetical prote	786	5	3.7	133	2	A29174	clostripain (EC 3.
714	5	3.7	122	2	H85623	ycgv protein - Esc	787	5	3.7	133	2	A82656	hypothetical prote
715	5	3.7	122	2	A05175	hypothetical prote	788	5	3.7	133	2	B97270	CBS domain contain
716	5	3.7	122	4	UN01029	serum amyloid A3 p	789	5	3.7	133	2	AH2580	PTS system, IIA co
717	5	3.7	123	2	T14949	hypothetical prote	790	5	3.7	133	2	F97362	PTS enzyme IIAB, m
718	5	3.7	123	2	H72479	probable translati	791	5	3.7	133	2	AE1971	hypothetical prote
719	5	3.7	124	2	T09855	acetyl-CoA carboxy	792	5	3.7	134	2	SL4076	Ig kappa chain - A
720	5	3.7	124	2	H72766	hypothetical prote	793	5	3.7	134	2	S43470	fatty-acid-binding
721	5	3.7	124	2	H72496	hypothetical prote	794	5	3.7	134	2	AD0323	NrdI protein homol
722	5	3.7	124	2	A83505	hypothetical prote	795	5	3.7	134	2	F84174	hypothetical prote
723	5	3.7	124	2	H86143	hypothetical prote	796	5	3.7	134	2	A40227	transcription repr
724	5	3.7	124	2	A72587	hypothetical prote	797	5	3.7	134	2	JC2112	helix-loop-helix p
725	5	3.7	125	2	F96973	transcription regu	798	5	3.7	135	2	H71499	hypothetical prote
726	5	3.7	125	2	B72517	hypothetical prote	799	5	3.7	135	2	C95375	hypothetical prote
727	5	3.7	125	2	D75313	hypothetical prote	800	5	3.7	135	2	H84968	flagella synthesis
728	5	3.7	125	2	C75507	hypothetical prote	801	5	3.7	135	2	H86417	probable auxin-ind
729	5	3.7	126	2	T00310	transposase - Esch	802	5	3.7	136	2	B65210	Yjba protein - Esc
730	5	3.7	126	2	A82575	hypothetical prote	803	5	3.7	136	2	T23859	hypothetical prote
731	5	3.7	127	2	B82817	translation initia	804	5	3.7	136	2	B96504	protein F9C16.21 l
732	5	3.7	127	2	T03866	hypothetical prote	805	5	3.7	136	2	F84890	hypothetical prote
733	5	3.7	127	2	A10894	probable exported	806	5	3.7	136	2	T32161	hypothetical prote
734	5	3.7	127	2	T07301	cell division topo	807	5	3.7	136	2	B97386	hypothetical prote
735	5	3.7	127	2	G72604	hypothetical prote	808	5	3.7	137	1	S25968	succinate dehydrog
736	5	3.7	127	2	D97449	hypothetical prote	809	5	3.7	137	2	D24773	protein-tyrosine k
737	5	3.7	127	2	AG2667	conserved hypothet	810	5	3.7	137	2	S43885	3-isopropylmalate
738	5	3.7	127	2	A83162	hypothetical prote	811	5	3.7	137	2	JQ2325	virion protein - A
739	5	3.7	127	2	A11362	hypothetical prote	812	5	3.7	137	2	A45355	ORF7 protein - Aut
740	5	3.7	127	2	PN0464	hypothetical prote	813	5	3.7	137	2	G81659	hypothetical prote
741	5	3.7	127	2	A48420	pheromone 4 praeur	814	5	3.7	137	2	H90342	hypothetical prote
742	5	3.7	128	1	C8EC62	cytochrome b562 pr	815	5	3.7	138	2	S36567	E6 protein - human
743	5	3.7	128	2	AF1056	soluble cytochrome	816	5	3.7	138	2	D85665	hypothetical prote
744	5	3.7	128	2	D64607	diacylglycerol kin	817	5	3.7	138	2	S70784	curli assembly/tra
745	5	3.7	128	2	G72763	hypothetical prote	818	5	3.7	138	2	G90805	curli assembly/tra
746	5	3.7	128	2	A70112	hypothetical prote	819	5	3.7	138	2	F98236	ornithine cyclodea
747	5	3.7	128	2	H65171	hypothetical trans	820	5	3.7	139	2	B97709	hypothetical prote
748	5	3.7	128	2	G31250	hypothetical prote	821	5	3.7	139	2	D86417	probable auxin-ind
749	5	3.7	128	2	B93492	hypothetical prote	822	5	3.7	139	2	E96030	conserved hypothet
750	5	3.7	128	2	B72600	hypothetical prote	823	5	3.7	140	2	S54215	flhE protein - Yer
751	5	3.7	129	2	S78153	ribosomal protein	824	5	3.7	140	2	AF0218	flagellar protein
752	5	3.7	129	2	A81980	hypothetical prote	825	5	3.7	140	2	S43789	probable cell wall
753	5	3.7	129	2	S73744	Mg296 homolog A05	826	5	3.7	140	2	D84594	hypothetical prote
754	5	3.7	129	2	AH2003	hypothetical prote	827	5	3.7	140	2	F86886	conserved hypothet
755	5	3.7	129	2	A82728	hypothetical prote	828	5	3.7	140	2	T35301	hypothetical prote
756	5	3.7	129	2	E84564	hypothetical prote	829	5	3.7	141	2	S31685	Ig heavy chain V r
757	5	3.7	129	2	T35391	probable transcrip	830	5	3.7	141	2	A91249	probable transcrip
758	5	3.7	129	2	T28983	hypothetical prote	831	5	3.7	141	2	T35223	probable ATP/Grp b
759	5	3.7	129	2	F72425	2-amino-4-hydroxy-	832	5	3.7	141	2	T13642	probable holin - S

833	5	3.7	141	2	AB0042	probable exported	906	5	3.7	151	2	C75157	protein tyrosine p
834	5	3.7	141	2	A70650	hypothetical prote	907	5	3.7	152	2	D82911	probable H1t prote
835	5	3.7	142	2	S73213	ribosomal protein	908	5	3.7	152	2	A95883	probable aldehyde
836	5	3.7	142	2	S71071	lsu ribosomal prot	909	5	3.7	152	2	T11658	mitochondrial impo
837	5	3.7	142	2	B71043	probable ribosomal	910	5	3.7	153	2	T04614	hypothetical prote
838	5	3.7	142	2	B75463	conserved hypothe	911	5	3.7	153	2	G82778	hypothetical prote
839	5	3.7	142	2	C75344	conserved hypothe	912	5	3.7	153	2	E90091	hypothetical prote
840	5	3.7	142	2	G72050	conserved hypothe	913	5	3.7	153	2	B83143	probable acetyltra
841	5	3.7	142	2	D86574	CR550 hypothetical	914	5	3.7	153	2	H72777	hypothetical prote
842	5	3.7	142	2	A87501	hypothetical prote	915	5	3.7	153	2	AG1363	hypothetical prote
843	5	3.7	142	2	A12479	hypothetical prote	916	5	3.7	154	1	D69425	conserved hypothe
844	5	3.7	142	2	B44355	CD44 glycoprotein	917	5	3.7	154	2	S72939	hypothetical prote
845	5	3.7	142	2	S46445	YMF46 protein - AC	918	5	3.7	154	2	G70724	hypothetical prote
846	5	3.7	142	2	AH1242	comG operon protei	919	5	3.7	154	2	T03503	conserved hypothe
847	5	3.7	143	2	S45537	peptidylprolyl iso	920	5	3.7	154	2	C93339	transcription regu
848	5	3.7	143	2	A69115	hypothetical prote	921	5	3.7	155	2	C83460	cytochrome C-type
849	5	3.7	143	2	F86168	hypothetical prote	922	5	3.7	155	2	H82879	ribosomal protein
850	5	3.7	143	2	T45347	hypothetical prote	923	5	3.7	155	2	S61835	cheW protein - Rhi
851	5	3.7	143	2	E70780	hypothetical prote	924	5	3.7	155	2	C75191	transcription regu
852	5	3.7	144	2	G86293	40S ribosomal prot	925	5	3.7	155	2	H84066	hypothetical prote
853	5	3.7	144	2	E84728	40S ribosomal prot	926	5	3.7	155	2	B97207	probable acetyltra
854	5	3.7	144	2	A83270	hypothetical prote	927	5	3.7	155	2	B71223	hypothetical prote
855	5	3.7	144	2	H81570	conserved hypothe	928	5	3.7	156	1	D43735	cellulose biosynth
856	5	3.7	144	2	A95285	hypothetical prote	929	5	3.7	156	2	PD0017	fertility restore
857	5	3.7	144	4	I51936	hypothetical BCR/A	930	5	3.7	156	2	E64084	kdtB protein - Hae
858	5	3.7	145	2	I39505	gene aac(6')-Ii pr	931	5	3.7	156	2	G69233	N-terminal acetyl
859	5	3.7	145	2	I39502	aminoglycoside 6'	932	5	3.7	156	2	AF2149	hypothetical prote
860	5	3.7	145	2	AG3271	LSU ribosomal prot	933	5	3.7	156	2	T32427	hypothetical prote
861	5	3.7	145	2	C83323	probable transcrip	934	5	3.7	156	2	A87366	hypothetical prote
862	5	3.7	145	2	F85690	hypothetical prote	935	5	3.7	156	2	D96706	unknown protein, 5
863	5	3.7	145	2	A70576	hypothetical prote	936	5	3.7	156	2	D70541	hypothetical prote
864	5	3.7	145	2	S30402	hypothetical prote	937	5	3.7	156	4	A24847	hypothetical BCR/A
865	5	3.7	145	2	AC0538	hypothetical prote	938	5	3.7	157	2	D72296	VP29-like phospho
866	5	3.7	145	2	AC2452	hypothetical prote	939	5	3.7	157	2	A53874	protein-tyrosine-p
867	5	3.7	145	2	B96705	unknown protein, 8	940	5	3.7	157	2	B53874	protein-tyrosine-p
868	5	3.7	145	2	E75490	hypothetical prote	941	5	3.7	157	2	E84220	molybdenum cofacto
869	5	3.7	145	2	A13048	transcription regu	942	5	3.7	157	2	AF0606	probable membrane
870	5	3.7	145	2	B98237	probable regulator	943	5	3.7	157	2	S58338	hypothetical prote
871	5	3.7	146	2	I39504	gene aac(6')-Ij pr	944	5	3.7	157	2	D72535	hypothetical prote
872	5	3.7	146	2	I39503	gene aac(6')-Ih pr	945	5	3.7	157	2	AH0939	probable membrane
873	5	3.7	146	2	S51810	trypsin inhibitor	946	5	3.7	157	2	AC1215	hypothetical prote
874	5	3.7	146	2	S51811	trypsin inhibitor	947	5	3.7	157	2	AG1568	hypothetical prote
875	5	3.7	146	2	S75815	hypothetical prote	948	5	3.7	158	2	S02758	retinoic acid rece
876	5	3.7	146	2	D95986	hypothetical prote	949	5	3.7	158	2	A71101	hypothetical prote
877	5	3.7	146	2	A95342	hypothetical prote	950	5	3.7	158	2	AI2899	conserved hypothe
878	5	3.7	146	2	AH1935	transcription regu	951	5	3.7	158	2	B97675	hypothetical prote
879	5	3.7	147	2	I51014	MHC class I protei	952	5	3.7	158	2	E87723	protein R06A10.3 [
880	5	3.7	147	2	D69008	conserved hypothe	953	5	3.7	158	2	B84588	probable AP2 domai
881	5	3.7	147	2	D71540	hypothetical prote	954	5	3.7	158	2	T00933	RNA-binding protei
882	5	3.7	147	2	T21719	hypothetical prote	955	5	3.7	158	2	G95925	probable acetyltra
883	5	3.7	147	2	H90305	hypothetical prote	956	5	3.7	159	2	A11406	spermidine/spermin
884	5	3.7	147	2	D86389	hypothetical prote	957	5	3.7	159	2	A11782	spermidine/spermin
885	5	3.7	148	2	B97768	hypothetical prote	958	5	3.7	159	2	AE2547	hypothetical prote
886	5	3.7	148	2	A39106	ribosomal protein	959	5	3.7	160	2	T32026	hypothetical prote
887	5	3.7	148	2	T03569	hypothetical 16.9K	960	5	3.7	160	2	S76609	hypothetical prote
888	5	3.7	148	2	A86538	CT053 hypothetical	961	5	3.7	160	2	B81322	peptidylprolyl iso
889	5	3.7	148	2	H72085	conserved hypothe	962	5	3.7	160	2	T29392	hypothetical prote
890	5	3.7	149	2	C87666	ribonuclease Hi [i	963	5	3.7	160	2	B95973	hypothetical expor
891	5	3.7	149	2	G72250	ribosomal protein	964	5	3.7	160	2	AB3559	transcription regu
892	5	3.7	149	2	T35846	probable integral	965	5	3.7	161	1	Z3BP79	gene 49.1 protein
893	5	3.7	149	2	E95201	hypothetical prote	966	5	3.7	161	2	A29557	calcium-binding pr
894	5	3.7	149	2	E98068	hypothetical prote	967	5	3.7	161	2	A24921	calmodulin-like pr
895	5	3.7	149	2	H72746	hypothetical prote	968	5	3.7	161	2	AG3557	bacterioferritin [
896	5	3.7	149	2	S53876	sex-regulated prot	969	5	3.7	161	2	S68771	bacterioferritin -
897	5	3.7	150	2	A54581	ribosomal protein	970	5	3.7	161	2	G64636	hypothetical prote
898	5	3.7	150	2	JS0024	15K calcium-bindin	971	5	3.7	161	2	D71879	hypothetical prote
899	5	3.7	150	2	A72328	conserved hypothe	972	5	3.7	161	2	A69181	hypothetical prote
900	5	3.7	150	2	D97188	uncharacterized pr	973	5	3.7	161	2	F72593	hypothetical prote
901	5	3.7	150	2	T36099	hypothetical prote	974	5	3.7	161	2	AC3085	conserved hypothe
902	5	3.7	150	2	G84173	archaeal histone A	975	5	3.7	161	2	E98221	hypothetical 23.2K
903	5	3.7	151	2	A69195	transcription regu	976	5	3.7	162	1	A53484	interleukin-15 pre
904	5	3.7	151	2	C48956	thioesterase - Art	977	5	3.7	162	1	TDMS	Thy-1 membrane gly
905	5	3.7	151	2	C84600	hypothetical prote	978	5	3.7	162	2	T50253	Vacuolar ATP synth

979 5 3.7 162 2 JC7157 calcium vector pro
980 5 3.7 162 2 A87591 cytochrome c-type
981 5 3.7 162 2 A24442 hypothetical prote
982 5 3.7 163 1 D69840 conserved hypothet
983 5 3.7 163 2 A72762 probable bacteriof
984 5 3.7 163 2 E69133 conserved hypothet
985 5 3.7 163 4 I39436 hypothetical BCR/A
986 5 3.7 164 2 H72231 ATP synthase F0, s
987 5 3.7 164 2 C84777 cyclophilin-like p
988 5 3.7 164 2 T29903 hypothetical prote
989 5 3.7 164 2 S52279 glutamate uptake r
990 5 3.7 164 2 JQ1252 hypothetical 16.7K
991 5 3.7 164 2 C70144 hypothetical prote
992 5 3.7 164 2 S35220 hypothetical prote
993 5 3.7 165 2 H84997 hypothetical prote
994 5 3.7 165 2 D81811 hypothetical prote
995 5 3.7 165 2 F82452 conserved hypothet
996 5 3.7 165 2 G30338 comG operon protei
997 5 3.7 165 2 A28138 interferon-induced
998 5 3.7 166 2 T45703 ubiquitin-protein
999 5 3.7 166 2 T43497 hypothetical prote
1000 5 3.7 166 2 A38122 ard protein - Bsch

ALIGNMENTS

RESULT 1
A69898 conserved hypothetical protein yozA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69898
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, J.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Satoh, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Segnuchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: A69898
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-210 <KUN>
A;Cross-references: UNIPROT:O34947; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13771.
A;Experimental source: strain 168
C;Genetics:
A;Gene: yozA

Query Match 5.9%; Score 8; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 LANEGYLN 121
|||||||
Db 116 LANEGYLN 123

RESULT 2
T36718 probable integral membrane protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36718

R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21612
A;Accession: T36718
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-253 <MUR>
A;Cross-references: UNIPROT:Q9XA15; EMBL:AL079308; PIDN:CAB45216.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE8B:SCH69.19c

Query Match 5.2%; Score 7; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 65 LPETSKY 71
|||||||
Db 188 LPETSKY 194

RESULT 3
C72418 hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: C72418
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72418
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <ARN>
A;Cross-references: UNIPROT:Q9WXV4; GB:AE001696; GB:AE000512; NID:g4980582; PIDN:AAD3519.
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0099
C;Superfamily: Thermotoga maritima hypothetical protein TM0099

Query Match 5.2%; Score 7; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 VFLELSA 63
|||||||
Db 166 VFLELSA 172

RESULT 4
H75032 hypothetical protein PAB0826 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H75032
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: H75032
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-285 <KAW>
A;Cross-references: UNIPROT:Q9UZA2; GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB5015.
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB0826

Query Match 5.2%; Score 7; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 YVLSVFL 59
|||||
Db 25 YVLSVFL 31

RESULT 5
T27194
hypothetical protein Y57A10B.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27194
R:Smyle, R.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20326
A:Accession: T27194
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-316 <WIL>
A:Cross-references: UNIPROT:Q9XWH8; EMBL:AL032647; PIDN:CAA21690.1; GSPDB:GN000019; CBSP:
A:Experimental source: clone Y57A10B
C:Genetics:
A:Gene: CESP:Y57A10B.3
A:Map position: 1
A:Introns: 54/2; 174/3; 226/1
C:Superfamily: *Caenorhabditis elegans* hypothetical protein K02E7.9

Query Match 5.2%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 SVFLELS 62
|||||
Db 295 SVFLELS 301

RESULT 6
AC3426
mannosyltransferase C (EC 2.4.1.-) [imported] - *Brucella melitensis* (strain 16M)
C:Species: *Brucella melitensis*
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AC3426
R:DeIvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A:Reference number: AD3252; PMID:11756688
A:Accession: AC3426
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <KUP>
A:Cross-references: UNIPROT:Q8YFW9; GB:AE008917; PIDN:AAL52574.1; PID:gl79833391; GSPDB:G
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1393
A:Map position: 1
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 5.2%; Score 7; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 LELSAGL 65
|||||
Db 269 LELSAGL 275

RESULT 7
T35794
probable 4-aminobutyrate aminotransferase - *Streptomyces coelicolor*
C:Species: *Streptomyces coelicolor*
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C:Accession: T35794
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z21556
A:Accession: T35794
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-444 <MUR>
A:Cross-references: UNIPROT:O86823; EMBL:AL031225; PIDN:CAA20213.1; GSPDB:GN000070; SCORE
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: gabT; SCORDB:SCB87.02
C:Superfamily: ornithine-oxo-acid aminotransferase

Query Match 5.2%; Score 7; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 IREFASD 96
|||||
Db 245 IREFASD 251

RESULT 8
T48645
glycine betaine transport protein betL [validated] - *Listeria monocytogenes*
C:Species: *Listeria monocytogenes*
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48645
R:Sleator, R.D.; Gahan, C.G.M.; Abee, T.; Hill, C.
Appl. Environ. Microbiol. 65, 2078-2083, 1999
A:Title: Identification and disruption of betL, a secondary glycine betaine transport sy
A:Reference number: 224496; MUID:99240434; PMID:10224004
A:Accession: T48645
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-507 <SLE>
A:Cross-references: UNIPROT:Q9X4A5; EMBL:AF102174; NID:g4850173; PIDN:AAD30266.1; PID:g4
A:Experimental source: strain L028
C:Genetics:
A:Gene: betL
C:Function:
A:Description: responsible for glycine betaine uptake [validated, MUID:99240434]; seems
C:Superfamily: *Escherichia coli* probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
|||||
Db 415 DSATFVL 421

RESULT 9
AD1336
glycine betaine transporter BetL betL [imported] - *Listeria monocytogenes* (strain EGD-e)
C:Species: *Listeria monocytogenes*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD1336
R:Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1336
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-507 <GLA>
A:Cross-references: UNIPROT:Q9X4A5; GB:NC_003210; PIDN:CAD00170.1; PID:gl6411562; GSPDB:

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: betL

C;Superfamily: Escherichia coli probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13

Db 415 DSATFVL 421

RESULT 10

AB1707
glycine betaine transporter BetL [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AB1707

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, P.; Berche, P.; Bloeker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluecker, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AB1707

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-507 <GLA>

A;Cross-references: UNIPROT:Q929S7; GB:ALU592022; PIDN:CAC97426.1; PID:glc414710; GSPDB:G

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: betL

C;Superfamily: Escherichia coli probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13

Db 415 DSATFVL 421

RESULT 11

G69670

glycine betaine transporter opuD - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: G69670

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Enian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleg

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maunda, S.; Maue

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleith, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: Ae9580; MUID:98044033; PMID:9384377

A;Accession: G69670

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-512 <KUN>

A;Cross-references: UNIPROT:P54417; GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14985.
A;Experimental source: strain 168

C;Genetics:

A;Gene: opuD

C;Superfamily: Escherichia coli probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13

Db 416 DSATFVL 422

RESULT 12

E89910

glycine betaine transporter opuD [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: E89910

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: E89910

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-548 <KUR>

A;Cross-references: UNIPROT:Q99UC9; GB:BA000018; PID:gl3701146; PIDN:BA842441.1; GSPDB:G

A;Experimental source: strain N315

C;Genetics:

A;Gene: opuD

C;Superfamily: Escherichia coli probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13

Db 423 DSATFVL 429

RESULT 13

C84534

hypothetical protein At2g15880 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: C84534

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; I

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84534

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-727 <STO>

A;Cross-references: UNIPROT:Q9XIL9; GB:A8002093; NID:95306245; PIDN:AD41978.1; GSPDB:GN

A;Gene: At2g15880

A;Map position: 2

Query Match 5.2%; Score 7; DB 2; Length 727;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 PVYSPPL 31

Db 423 DSATFVL 429

Db 665 PVSPPL 671

RESULT 14

F96586

hypotheical protein F20D21.29 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: F96586

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Lin, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96586

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-818 <STO>

A:Cross-references: UNIPROT:Q9SLI6; GB:AE005173; NID:G4585990; PIDN:AAD25626.1; GSPDB:GN

C:Genetics:

A:Gene: F20D21.29

A:Map position: 1

Query Match

5.2%; Score 7; DB 2; Length 818;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 LELSAGL 65

|||||

Db 111 LELSAGL 117

RESULT 15

T04377

probable pullulanase (EC 3.2.1.41) - barley

N:Alternate names: pullulanase

C:Species: Hordeum vulgare (barley)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T04377

R:Lok, F.; Kristensen, M.; Planchot, V.; Leah, R.; Svendsen, I.; Svenson, B.

submitted to the EMBL Data Library, December 1997

A:Description: Isolation and characterization of starch debranching enzyme, limit dextrin

A:Reference number: Z15320

A:Accession: T04377

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-904 <LOK>

A:Cross-references: UNIPROT:O48541; EMBL:AF022725; NID:G2502057; PIDN:AAD04189.1; PID:G2

A:Experimental source: cv. Igr1

C:Genetics:

A:Gene: HvLD99

A:Introns: 21/3; 70/1; 87/3; 124/1; 169/3; 235/2; 285/2; 305/3; 346/1; 376/2; 407/3; 439

C:Superfamily: pullulanase type debranching enzyme

C:Keywords: glycosidase; hydrolase

Query Match

5.2%; Score 7; DB 2; Length 904;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 SAGLPET 68

|||||

Db 81 SAGLPET 87

Search completed: July 20, 2005, 20:52:49

Job time : 20.2857 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:38:00 ; Search time 18.8571 Seconds
(without alignments)
673.517 Million cell updates/sec

Title: US-09-706-325-24

Perfect score: 132

Sequence: 1 SYMTINNFSCREEMGEVI.....EANGLLPDKLTLCFVSVV 132

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	30.3	409	2 S42384	Kruppel-like prote
2	7	5.3	136	1 B4956	flagellar protein
3	7	5.3	136	2 H9061	flagellar protein
4	7	5.3	136	2 H85809	hypothetical prote
5	7	5.3	143	2 A71051	hypothetical prote
6	7	5.3	145	2 F82133	hypothetical prote
7	7	5.3	296	2 J26050	homoserine kinase
8	7	5.3	296	2 H86769	homoserine kinase
9	7	5.3	302	2 H95075	hypothetical prote
10	7	5.3	304	2 D69744	conserved hypotet
11	7	5.3	310	2 C93088	hypothetical prote
12	7	5.3	311	2 A99196	purine nucleosidas
13	7	5.3	325	2 T45994	hypothetical prote
14	7	5.3	331	2 G75540	Elac family protei
15	7	5.3	340	2 G69474	conserved hypotet
16	7	5.3	401	2 E85253	hypothetical prote
17	7	5.3	421	2 I49734	HNF-3/foxa-head ho
18	7	5.3	441	2 B48454	hypothetical prote
19	7	5.3	563	1 C64420	N-methylhydantoina
20	7	5.3	567	2 J55338	Rab geranylgeranyl
21	7	5.3	567	2 A45977	Rab geranylgeranyl
22	7	5.3	583	1 A29576	H+/K+-exchanging A
23	7	5.3	660	2 H70798	probable cation-tr
24	7	5.3	684	2 E97943	Na+/H+ antiporter
25	7	5.3	745	1 B45995	copper-transportin
26	7	5.3	774	1 P31V50	RNA-directed RNA p
27	7	5.3	774	2 S13670	basic polymerase 2
28	7	5.3	817	2 S77106	hypothetical prote
29	7	5.3	844	2 C86339	protein PD10.12 [

alpha-mannosidase
hypothetical prote
lipophorin - fruit
ribosomal protein
hypothetical prote
hypothetical prote
regulatory protein
granulocyte chemot
nulin ENOD40, ea
hypothetical prote
Bkm-like sex-deter
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical 10.6K
NADH2 dehydrogenas
plastocyanin b - L
multidrug resistanc
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypotet
hypothetical prote
conserved hypotet
CT550 hypothetical
ribosomal protein
hypothetical prote
probable protein t
ribosomal protein
probable furA prot
T-cell receptor be
clathrin-associate
elicitor responsiv
calmodulin-related
polyferredoxin 2x2
T-cell receptor be
early protein gp17
hypothetical prote
hypothetical prote
plastocyanin a pre
plastocyanin b pre
hypothetical prote
hypothetical prote
ribosome releasing
ribosome recycling
probable NDP-4-ket
adenylate kinase [
probable 60S ribos
60S ribosomal prot
F12P19.3 [imported
precorrin decarbox
hypothetical prote
adenylate kinase (
glutathione transf
hypothetical prote
transcription regu
coat protein - Bry
Maf/YceF/YhdE fami
probable membrane
hypothetical prote
ribosomal protein
conserved hypotet
ribosomal protein
ribosomal protein
hypothetical prote
ribosomal protein
hypothetical secre

103	6	4.5	216	2	S04207	sporamin B (clone	176	6	4.5	304	2	D70370	hypothetical prote
104	6	4.5	216	2	S07466	sporamin B precursor	177	6	4.5	305	2	A70482	ABC transporter -
105	6	4.5	216	2	A30835	sporamin precursor	178	6	4.5	307	2	D69521	hypothetical prote
106	6	4.5	218	2	S49596	ribosomal protein	179	6	4.5	308	2	I56573	synaptic glycoprot
107	6	4.5	219	2	S07465	sporamin A precursor	180	6	4.5	308	2	T50639	synaptic glycoprot
108	6	4.5	219	2	S04208	sporamin A (clone	181	6	4.5	308	2	T50638	synaptic glycoprot
109	6	4.5	219	2	E60110	repetitive protein	182	6	4.5	310	2	H90465	alcohol dehydrogen
110	6	4.5	219	2	E82825	hypothetical prote	183	6	4.5	313	2	D86219	protein F22013.19
111	6	4.5	220	2	E86277	hypothetical prote	184	6	4.5	313	2	F64089	survival protein s
112	6	4.5	220	2	T02068	probable transcrip	185	6	4.5	315	2	T46156	hypothetical prote
113	6	4.5	220	2	J02244	ribosomal protein	186	6	4.5	315	2	C81962	probable inner mem
114	6	4.5	220	2	A38575	gluconate 2-dehydr	187	6	4.5	316	2	T46000	hypothetical prote
115	6	4.5	220	2	S51444	hypothetical prote	188	6	4.5	316	1	F70536	3',5'-cyclic-nucle
116	6	4.5	221	2	A86396	60s ribosomal prot	189	6	4.5	318	2	F70822	hypothetical prote
117	6	4.5	223	1	C5NCM	peptidylprolyl iso	190	6	4.5	319	2	S73159	hypothetical prote
118	6	4.5	224	2	S49575	ribosomal protein	191	6	4.5	320	1	S20014	ubiquinol-cytochro
119	6	4.5	225	2	S57810	hypothetical prote	192	6	4.5	322	2	AG3207	conserved hypothet
120	6	4.5	225	2	T36733	probable transcrip	193	6	4.5	322	2	AG1929	hypothetical prote
121	6	4.5	226	1	LCRT	prolactin precursor	194	6	4.5	324	2	S28672	occR protein - Agr
122	6	4.5	228	2	T07957	probable ribosomal	195	6	4.5	324	2	F81018	iron(III) ABC tran
123	6	4.5	229	1	BVECHJ	molybdenum transpo	196	6	4.5	329	2	AG3055	succinoglycan bios
124	6	4.5	229	2	A00595	molybdenum transpo	197	6	4.5	332	2	C95150	SAP domain protein
125	6	4.5	229	2	H30727	molybdate transpor	198	6	4.5	334	2	T11633	hypothetical prote
126	6	4.5	229	2	A85579	molybdate transpor	199	6	4.5	334	2	E71706	hypothetical prote
127	6	4.5	231	2	A23466	hypothetical prote	200	6	4.5	334	2	S48136	delichyl-phosphate
128	6	4.5	231	2	S50517	hypothetical prote	201	6	4.5	337	2	F98230	succinoglycan bios
129	6	4.5	232	2	G97109	response regulator	202	6	4.5	338	2	A96769	protein flavonol s
130	6	4.5	232	2	A35967	probable two compo	203	6	4.5	338	2	F84146	cytochrome d ubiqu
131	6	4.5	233	2	C72105	conserved hypothet	204	6	4.5	339	2	G90311	acetoin catabolism
132	6	4.5	233	2	D86519	disulfide bond cha	205	6	4.5	341	2	AC3469	ABC transporter su
133	6	4.5	235	2	AG2170	hypothetical prote	206	6	4.5	345	2	G69138	conserved hypothet
134	6	4.5	238	1	S28674	hypothetical prote	207	6	4.5	348	2	S40750	hypothetical prote
135	6	4.5	238	2	D84827	probable protein k	208	6	4.5	353	2	S28548	protein kinase (EC
136	6	4.5	239	2	G84889	hypothetical prote	209	6	4.5	355	2	H95159	3-dehydroquinat s
137	6	4.5	239	2	S68257	phospholipase C (E	210	6	4.5	355	2	H98025	3-dehydroquinat s
138	6	4.5	239	2	H64343	hypothetical prote	211	6	4.5	356	2	C97010	hypothetical prote
139	6	4.5	241	2	D89928	hypothetical prote	212	6	4.5	356	2	T38408	conserved hypothet
140	6	4.5	242	2	F95256	ABC transporter, A	213	6	4.5	360	2	B90239	hypothetical prote
141	6	4.5	242	2	G98121	hypothetical prote	214	6	4.5	361	2	H96594	hypothetical prote
142	6	4.5	244	2	A75408	triosephosphate is	215	6	4.5	362	1	JQ0735	recF protein - Pro
143	6	4.5	245	2	D97148	enoyl-CoA hydratase	216	6	4.5	366	2	T16249	hypothetical prote
144	6	4.5	246	2	E90309	hypothetical prote	217	6	4.5	367	2	T23387	hypothetical prote
145	6	4.5	250	2	C64304	ABC transporter su	218	6	4.5	367	2	A42937	probable transposa
146	6	4.5	251	2	B64337	hypothetical prote	219	6	4.5	368	2	E64142	hypothetical prote
147	6	4.5	253	2	JC5511	TATA-binding prote	220	6	4.5	368	2	G82870	Grp-binding protei
148	6	4.5	255	2	A81935	hypothetical prote	221	6	4.5	372	2	D81413	probable secreted
149	6	4.5	257	2	F88904	protein Y57G11C.3	222	6	4.5	372	2	S60207	fomF protein - Str
150	6	4.5	258	2	E90126	hypothetical prote	223	6	4.5	381	2	T28378	ORF MSV217 SCG gen
151	6	4.5	261	2	A60454	hypothetical prote	224	6	4.5	383	2	C90136	26S proteasome SU
152	6	4.5	261	2	H83848	cobalamin synthase	225	6	4.5	383	2	A96590	hypothetical prote
153	6	4.5	261	2	B83672	hypothetical prote	226	6	4.5	385	2	F75168	2-ketoglutarate fe
154	6	4.5	264	2	I39141	transcription fact	227	6	4.5	386	2	A96532	hypothetical prote
155	6	4.5	269	2	T27244	hypothetical prote	228	6	4.5	390	2	D83057	probable aminotran
156	6	4.5	269	2	B84429	hypothetical prote	229	6	4.5	390	2	AH2904	conserved hypothet
157	6	4.5	270	2	F89623	flagellar basal-bo	230	6	4.5	391	2	T34935	hypothetical prote
158	6	4.5	275	2	T37304	ras GTPase-activat	231	6	4.5	391	2	F82369	conserved hypothet
159	6	4.5	278	2	A47090	urease-associated	232	6	4.5	392	2	AD1485	ABC transporter, A
160	6	4.5	279	2	B70115	translation elonga	233	6	4.5	393	2	AE3164	conserved hypothet
161	6	4.5	279	2	I64215	hypothetical prote	234	6	4.5	395	2	E97037	hypothetical prote
162	6	4.5	283	2	G70456	formyltetrahydrofo	235	6	4.5	396	1	TSEBBT	tryptophan synthas
163	6	4.5	284	2	S74352	phosphoribosylglyc	236	6	4.5	396	2	AF0268	tryptophan synthas
164	6	4.5	286	2	T02641	probable C2H2-type	237	6	4.5	396	2	S09627	prxR protein - Esc
165	6	4.5	290	2	D64335	nucleotide-binding	238	6	4.5	396	2	E83393	RND multidrug effl
166	6	4.5	291	2	T49260	hypothetical prote	239	6	4.5	396	2	T52445	hypothetical prote
167	6	4.5	294	2	T41953	G protein-coupled	240	6	4.5	396	2	S56954	protein YBR162c ho
168	6	4.5	295	2	H71306	probable cell divi	241	6	4.5	397	1	TSECB	tryptophan synthas
169	6	4.5	295	2	T00725	hypothetical prote	242	6	4.5	397	2	T47190	tryptophan synthas
170	6	4.5	295	2	F84456	hypothetical prote	243	6	4.5	397	2	AC0653	tryptophan synthas
171	6	4.5	298	2	H96584	hypothetical prote	244	6	4.5	397	2	G85761	tryptophan synthas
172	6	4.5	299	2	A39497	heterodisulfide re	245	6	4.5	397	2	A99858	tryptophan synthas
173	6	4.5	300	2	C69857	formyltetrahydrofo	246	6	4.5	398	2	H70393	hemolysin - Aquife
174	6	4.5	300	2	D83158	hypothetical prote	247	6	4.5	399	2	T32933	hypothetical prote
175	6	4.5	301	2	S73347	probable lipoprote	248	6	4.5	399	2	AC2785	MPS permease [drug

249	6	4.5	399	2	D97564	hypothetical prote	322	6	4.5	519	2	S36471	L2 protein - human
250	6	4.5	400	2	D28414	ORF MSV53 leucine	323	6	4.5	520	2	S36495	L2 protein - human
251	6	4.5	405	2	D75135	hypothetical prote	324	6	4.5	524	2	S29723	cytochrome P450 4F
252	6	4.5	406	1	S48220	serine-type D-Ala-	325	6	4.5	524	2	S35551	transcription fact
253	6	4.5	407	2	S52148	amk protein - Erw	326	6	4.5	525	2	D70747	probable ffh prote
254	6	4.5	410	2	D83744	hypothetical prote	327	6	4.5	526	1	F5XR10	outer capsid prote
255	6	4.5	410	2	T15442	hypothetical prote	328	6	4.5	530	2	F87590	serine proteinase
256	6	4.5	414	2	A29835	SalI protein - Esc	329	6	4.5	530	2	F96491	hypothetical prote
257	6	4.5	416	2	S75445	proteinase rhoB (E	330	6	4.5	534	2	A37483	F protein - Muraya
258	6	4.5	419	2	D90025	molybdopterin bios	331	6	4.5	534	2	T39903	serine-rich protei
259	6	4.5	420	2	T42090	tryptophan synthas	332	6	4.5	535	2	S56261	probable membrane
260	6	4.5	423	2	I38056	nicotinic acetylch	333	6	4.5	540	2	C71260	hypothetical prote
261	6	4.5	424	2	AF0350	histidine-tRNA lig	334	6	4.5	546	2	C56976	transfer complex p
262	6	4.5	424	2	B90083	gamma-tubulin [imp	335	6	4.5	549	1	D30010	cytochrome-c oxida
263	6	4.5	430	2	E84015	maltose/maltodextr	336	6	4.5	551	2	A11093	oligopeptide ABC t
264	6	4.5	430	2	S28707	hypothetical prote	337	6	4.5	551	2	AG1456	oligopeptide ABC t
265	6	4.5	436	2	G86009	probable cell-surf	338	6	4.5	551	2	TL3994	envelope protein -
266	6	4.5	439	2	T05134	hypothetical prote	339	6	4.5	553	1	S29861	hybrid cluster [4F
267	6	4.5	439	2	E70371	apolipoprotein N-a	340	6	4.5	553	2	D84133	exo-alpha-1,4-gluc
268	6	4.5	441	2	T50436	hypothetical prote	341	6	4.5	553	2	F89960	hypothetical prote
269	6	4.5	444	1	D72631	probable IMP dehyd	342	6	4.5	554	2	H70011	exo-alpha-1,4-gluc
270	6	4.5	446	2	B97680	hypothetical prote	343	6	4.5	555	2	A43784	Xpo protein - Afri
271	6	4.5	447	2	F37828	conserved GTP-bind	344	6	4.5	559	2	A99237	hypothetical prote
272	6	4.5	447	2	H71673	hypothetical prote	345	6	4.5	560	2	S29859	rosetasome alpha
273	6	4.5	451	2	AG1141	hypothetical prote	346	6	4.5	565	2	T29718	hypothetical prote
274	6	4.5	451	2	AB1500	hypothetical prote	347	6	4.5	566	2	A86483	protein F5J5.13 [i
275	6	4.5	452	2	G90654	hypothetical prote	348	6	4.5	567	2	C64478	hypothetical prote
276	6	4.5	452	2	G85505	hypothetical prote	349	6	4.5	568	1	WZMCC	pectate lyase (EC
277	6	4.5	454	2	E84745	regulatory protein	350	6	4.5	568	2	S28792	pectate lyase (EC
278	6	4.5	454	2	T43069	probable serine pr	351	6	4.5	570	2	T04836	probable serine/th
279	6	4.5	455	2	C95049	acetyl-CoA carboxy	352	6	4.5	573	2	C96806	hypothetical prote
280	6	4.5	455	2	A97920	biotin carboxylase	353	6	4.5	575	2	S72283	DNA-directed RNA p
281	6	4.5	455	2	S51116	nicotinic acetylch	354	6	4.5	579	2	AF2094	hypothetical prote
282	6	4.5	455	2	A55972	nicotinic acetylch	355	6	4.5	580	2	T37664	hypothetical prote
283	6	4.5	461	2	AC0827	probable sensor ki	356	6	4.5	581	2	F97184	DNA modification m
284	6	4.5	462	2	S10439	DNA-directed RNA p	357	6	4.5	582	1	ERADF2	fiber protein - hu
285	6	4.5	464	2	A33523	nicotinic acetylch	358	6	4.5	585	2	T48513	hypothetical prote
286	6	4.5	467	2	AD2440	protechlorophyllid	359	6	4.5	586	2	JC7277	Sarcophaga-derived
287	6	4.5	467	2	A89899	heat shock protein	360	6	4.5	587	2	A84078	two-component sens
288	6	4.5	468	2	T49117	glucosidase like p	361	6	4.5	591	1	CBBY2	L-lactate dehydrog
289	6	4.5	468	2	T21331	hypothetical prote	362	6	4.5	593	2	C97848	ABC transporter At
290	6	4.5	469	2	S74825	probable Rieske ir	363	6	4.5	594	2	T34855	probable glyoxylat
291	6	4.5	473	2	T04799	hypothetical prote	364	6	4.5	601	2	T51748	thimet oligopeptid
292	6	4.5	474	2	F97264	6-Phospho-Beta-D-G	365	6	4.5	608	2	T02684	MYB-related transc
293	6	4.5	476	2	A50479	starch synthase (E	366	6	4.5	611	2	JE0365	alkylglycerone-pho
294	6	4.5	477	2	JC7169	tubulointerstitial	367	6	4.5	612	2	H81043	hypothetical prote
295	6	4.5	477	2	B69194	2-oxoacid-ferredox	368	6	4.5	622	2	S61140	probable membrane
296	6	4.5	480	2	G71050	asparagine synthas	369	6	4.5	622	2	B86309	Similar to mudra p
297	6	4.5	481	1	T43809	methylaspartate mu	370	6	4.5	627	2	C69637	DNA gyrase-like pr
298	6	4.5	481	2	B85575	probable glutamate	371	6	4.5	629	2	T19563	hypothetical prote
299	6	4.5	481	2	B90724	probable glutamate	372	6	4.5	635	2	T37239	serotonin receptor
300	6	4.5	482	2	S86945	protein fJL162c -	373	6	4.5	640	2	S67656	hypothetical prote
301	6	4.5	483	2	A90176	NADH dehydrogenase	374	6	4.5	644	2	B97885	transporter, trunc
302	6	4.5	487	2	C97144	probable membrane	375	6	4.5	644	2	B85758	RNase II, mRNA deg
303	6	4.5	488	2	T02207	protein 21D7 - com	376	6	4.5	644	2	A64877	exoribonuclease II
304	6	4.5	488	2	C72334	hypothetical prote	377	6	4.5	644	2	C90861	RNase II, mRNA deg
305	6	4.5	489	2	S77357	hypothetical prote	378	6	4.5	645	2	T16078	hypothetical prote
306	6	4.5	492	2	F70326	conserved hypothet	379	6	4.5	654	2	S55262	hypothetical prote
307	6	4.5	493	2	S49175	legumain (EC 3.4.2	380	6	4.5	656	2	T41546	UV-endonuclease -
308	6	4.5	496	2	F91056	probable 2-compone	381	6	4.5	657	2	T41546	hypothetical prote
309	6	4.5	496	2	B85901	probable 2-compone	382	6	4.5	669	2	D72423	iron(II) transport
310	6	4.5	496	2	C65033	Putative sensor-li	383	6	4.5	671	2	D86479	hypothetical prote
311	6	4.5	499	2	T18699	hypothetical prote	384	6	4.5	672	2	S63043	MET4 protein - yea
312	6	4.5	499	2	T47722	probable protein k	385	6	4.5	682	2	B84021	two-component sens
313	6	4.5	501	2	D90395	conserved hypothet	386	6	4.5	683	2	T37240	serotonin receptor
314	6	4.5	501	2	D86815	xylokainase (EC 2	387	6	4.5	690	2	I51298	transforming prote
315	6	4.5	502	2	AG3641	histidine-tRNA lig	388	6	4.5	690	2	S62728	transposase - phag
316	6	4.5	505	2	S39962	endoglucanase - Er	389	6	4.5	691	2	A40024	regulatory protein
317	6	4.5	516	2	E86062	probable 2-compone	390	6	4.5	694	2	T01504	hypothetical prote
318	6	4.5	516	2	D91216	probable 2-compone	391	6	4.5	697	2	T37946	tryptophan synthas
319	6	4.5	516	2	J00872	hypothetical 56.2K	392	6	4.5	699	2	T14904	NADPH-ferrihemopro
320	6	4.5	516	2	F97541	methionyl-tRNA syn	393	6	4.5	699	2	A43734	probable protein k
321	6	4.5	516	2	AH2760	methionyl-tRNA syn	394	6	4.5	728	2	S43768	transcription acti

395	6	4.5	729	2	D72079	conserved hypothet	468	6	4.5	1466	2	T17138	ClfAA protein - ra
396	6	4.5	729	2	H86544	CT283 hypothetical	469	6	4.5	1467	2	T18411	latrophilin-1, bra
397	6	4.5	730	2	D29337	hypothetical prote	470	6	4.5	1471	2	T17149	latrophilin-1, bra
398	6	4.5	731	2	D36808	hypothetical prote	471	6	4.5	1472	2	T18413	latrophilin-1, bra
399	6	4.5	743	2	D84545	probable salt-indu	472	6	4.5	1501	2	S50992	SNQ2 protein - yea
400	6	4.5	743	2	C56695	transducin-like en	473	6	4.5	1510	2	T17145	ClfAB protein - ra
401	6	4.5	744	2	T13485	NADH2 dehydrogenas	474	6	4.5	1515	2	T17156	ClfBB protein - ra
402	6	4.5	744	2	G90124	hypothetical prote	475	6	4.5	1581	2	T32963	hypothetical prote
403	6	4.5	747	2	F88561	protein F58A4.11 [476	6	4.5	1649	2	T39938	hypothetical prote
404	6	4.5	761	2	S20458	pqqF protein - Kle	477	6	4.5	1683	2	S56811	probable membrane
405	6	4.5	765	2	H84247	adaptive-response	478	6	4.5	1706	2	I84499	zinc finger protei
406	6	4.5	776	2	T24262	hypothetical prote	479	6	4.5	1711	2	T21432	hypothetical prote
407	6	4.5	778	2	J27797	scallop unconvengi	480	6	4.5	1780	2	T17272	hypothetical prote
408	6	4.5	779	2	A57177	NIMA-like protein	481	6	4.5	1822	2	T14106	probable GPrase-ac
409	6	4.5	790	2	T19040	hypothetical prote	482	6	4.5	1868	2	T23707	hypothetical prote
410	6	4.5	795	2	D64343	hypothetical prote	483	6	4.5	1879	2	T19481	hypothetical prote
411	6	4.5	798	2	T41616	hypothetical prote	484	6	4.5	1921	2	T13827	kinesin-73 - fruit
412	6	4.5	805	2	AH2731	ATP-dependent prot	485	6	4.5	2026	1	OYBY	adenylate cyclase
413	6	4.5	805	2	G97512	ATP-dependent prot	486	6	4.5	2030	2	T33162	hypothetical prote
414	6	4.5	809	2	F81312	leucine-cRNA ligas	487	6	4.5	2161	1	A45389	genome polyprotein
415	6	4.5	811	2	B82365	glycerol-3-phospha	488	6	4.5	2231	2	D71870	hypothetical prote
416	6	4.5	811	2	T08738	hypothetical prote	489	6	4.5	2523	2	F70846	probable PPE prote
417	6	4.5	819	2	T19351	hypothetical prote	490	6	4.5	2657	2	T18497	hypothetical prote
418	6	4.5	832	2	T49494	condensin complex	491	6	4.5	2761	2	T29285	hypothetical prote
419	6	4.5	835	2	T15177	hypothetical prote	492	6	4.5	2774	2	A43359	microtubule-associ
420	6	4.5	839	2	E86260	protein T12C24.24	493	6	4.5	2960	2	A45259	desmoyokin - human
421	6	4.5	840	2	E96541	unknown protein [i	494	6	4.5	3972	2	S75251	hypothetical prote
422	6	4.5	845	2	D86301	F9IK19.8 protein -	495	6	4.5	4199	2	S76412	hypothetical prote
423	6	4.5	853	2	D95365	NADH2 dehydrogenas	496	6	4.5	4342	2	H83343	probable non-ribos
424	6	4.5	891	2	B82495	probable NADH dehy	497	6	4.5	4644	1	A38905	dyein heavy chain
425	6	4.5	935	2	S66306	hypothetical prote	498	5	3.8	10	2	A31571	hypertrehalosemic/
426	6	4.5	942	2	B27015	metalloproteinase,	499	5	3.8	11	2	PH0903	T-cell receptor be
427	6	4.5	942	2	C86610	insulinase family/	500	5	3.8	13	2	E53275	Ig kappa-1 chain J
428	6	4.5	954	2	I51703	c-kit-related kina	501	5	3.8	14	2	I64815	carbonic anhydrase
429	6	4.5	956	2	T19046	ras GPrase-activat	502	5	3.8	17	2	B42576	Hsp56 - bovine (fr
430	6	4.5	958	2	E83701	alpha-amylase G-6	503	5	3.8	17	2	A46218	ubiquinol-cytochro
431	6	4.5	967	2	T15680	hypothetical prote	504	5	3.8	20	2	A56045	urinary tract ston
432	6	4.5	993	2	D36812	protein F3F9.12 [i	505	5	3.8	21	2	I58423	arylhydrocarbon re
433	6	4.5	1003	2	A39521	Glycine dehydrogen	506	5	3.8	24	2	A43503	botulinum toxin ty
434	6	4.5	1003	2	T13856	kar protein - frui	507	5	3.8	27	2	I50388	myosin heavy chain
435	6	4.5	1018	1	GNWXG7	genome polypro-ein	508	5	3.8	27	2	H64520	hypothetical prote
436	6	4.5	1039	2	A85096	hypothetical prote	509	5	3.8	27	2	A05058	hypothetical prote
437	6	4.5	1048	2	T19045	ras GPrase-activat	510	5	3.8	30	2	E84786	hypothetical prote
438	6	4.5	1051	2	S27002	phospholipase C (E	511	5	3.8	31	2	S53289	gene X protein - h
439	6	4.5	1057	2	S09112	hypothetical prote	512	5	3.8	31	2	I48082	mitochondrial benz
440	6	4.5	1093	2	A47212	transcription fact	513	5	3.8	36	2	F22102	phycoerythrin-545
441	6	4.5	1128	2	T30296	R27-2 protein - Tr	514	5	3.8	39	2	AB0930	hypothetical prote
442	6	4.5	1137	2	D89610	Tocl protein - mou	515	5	3.8	39	2	AF0836	probable bacteriop
443	6	4.5	1141	2	T29104	ras GPrase-activat	516	5	3.8	39	2	F82226	hypothetical prote
444	6	4.5	1146	2	F84487	probable ABC trans	517	5	3.8	39	2	C97037	hypothetical prote
445	6	4.5	1165	2	A48667	peroxisomal assemb	518	5	3.8	40	2	C32338	hypothetical prote
446	6	4.5	1170	2	T19042	ras GPrase-activat	519	5	3.8	47	2	D97948	degenerate transpo
447	6	4.5	1186	2	A81294	pyruvate-flavodoxi	520	5	3.8	49	2	F82255	hypothetical prote
448	6	4.5	1189	2	S56852	hypothetical prote	521	5	3.8	51	2	I57670	folliotropin recept
449	6	4.5	1196	2	S65245	translation elonga	522	5	3.8	51	2	C81117	hypothetical prote
450	6	4.5	1207	2	C70013	conserved hypothet	523	5	3.8	51	2	C82658	hypothetical prote
451	6	4.5	1207	2	T19041	ras GPrase-activat	524	5	3.8	51	2	A11731	hypothetical gene
452	6	4.5	1217	2	A45493	phospholipase C-be	525	5	3.8	52	2	G97873	hypothetical prote
453	6	4.5	1219	2	T14578	nucleoporin Nup153	526	5	3.8	53	2	S10355	T-cell receptor be
454	6	4.5	1220	1	DJBEC3	DNA-directed DNA p	527	5	3.8	53	2	H80318	degenerate transpo
455	6	4.5	1220	2	T42573	hypothetical prote	528	5	3.8	54	2	D26506	complement C2 (EC
456	6	4.5	1224	2	T25770	hypothetical prote	529	5	3.8	54	2	A90543	hypothetical prote
457	6	4.5	1234	2	S20399	phospholipase C-be	530	5	3.8	54	2	T42318	hypothetical prote
458	6	4.5	1234	2	I38994	phospholipase C-be	531	5	3.8	54	2	H82199	FixS-related prote
459	6	4.5	1253	1	A44400	myosin heavy chain	532	5	3.8	55	2	E70593	probable rubA prot
460	6	4.5	1259	2	T19043	ras GPrase-activat	533	5	3.8	55	2	T11184	H+-transporting tw
461	6	4.5	1270	2	T22615	hypothetical prote	534	5	3.8	55	2	D95140	hypothetical prote
462	6	4.5	1302	2	T23236	hypothetical prote	535	5	3.8	55	2	T25692	hypothetical prote
463	6	4.5	1325	2	T01037	hypothetical prote	536	5	3.8	56	2	I53423	MHC class II DQ82
464	6	4.5	1336	2	T18288	ABC transport prot	537	5	3.8	56	2	S36812	probable synapse-a
465	6	4.5	1337	1	I38670	protein-tyrosine-p	538	5	3.8	56	2	G72592	hypothetical prote
466	6	4.5	1392	2	A43336	microtubule-vesicl	539	5	3.8	57	2	G97910	hypothetical prote
467	6	4.5	1427	2	S22695	restin - human	540	5	3.8	57	2	AH0423	probable membrane

541	5	3.8	58	2	S31551	ribulose-bisphosph	614	5	3.8	89	2	T08479	plasmid maintenanc
542	5	3.8	58	2	T13185	hypothetical prote	615	5	3.8	89	2	F82757	hypothetical prote
543	5	3.8	59	2	H91210	hypothetical prote	616	5	3.8	89	2	AH2853	hypothetical prote
544	5	3.8	59	2	F98276	hypothetical prote	617	5	3.8	90	2	C81917	hypothetical prote
545	5	3.8	60	2	I55550	low density lipopr	618	5	3.8	90	2	A81186	hypothetical prote
546	5	3.8	61	2	A21444	hypothetical prote	619	5	3.8	90	2	AB1207	B. subtilis Ykta p
547	5	3.8	63	2	A56886	natural killer enh	620	5	3.8	90	2	AI1563	B. subtilis Ykta p
548	5	3.8	63	2	T28361	ORF MSV200 hypothe	621	5	3.8	91	1	W5WL11	ESA protein - huma
549	5	3.8	65	2	E83492	hypothetical prote	622	5	3.8	91	1	W5WL6A	ESA protein - huma
550	5	3.8	67	2	C47036	archaeal histone H	623	5	3.8	91	2	B61055	ESA protein - huma
551	5	3.8	68	2	E69437	conserved hypothet	624	5	3.8	91	2	T24120	hypothetical prote
552	5	3.8	68	2	G69209	histone-related pr	625	5	3.8	91	2	E97841	hypothetical prote
553	5	3.8	69	2	S60826	M protein precursor	626	5	3.8	91	2	AC3075	sarcosine oxidase
554	5	3.8	69	2	A47036	histone-related pr	627	5	3.8	91	2	F98211	sarcosine oxidase
555	5	3.8	69	2	T48848	histone Hmf1 [limpo	628	5	3.8	92	2	FV0007	hypothetical prote
556	5	3.8	70	2	S76907	hypothetical prote	629	5	3.8	92	2	F90898	probable tail fibe
557	5	3.8	70	2	B64863	hypothetical prote	630	5	3.8	92	2	T14937	hypothetical prote
558	5	3.8	71	2	H64454	hypothetical prote	631	5	3.8	92	2	A85842	hypothetical prote
559	5	3.8	72	2	AG2418	hypothetical prote	632	5	3.8	93	2	A99311	small subunit of i
560	5	3.8	72	2	S30987	gene 42 protein -	633	5	3.8	93	2	D97144	hypothetical prote
561	5	3.8	72	2	T26975	hypothetical prote	634	5	3.8	93	2	D97144	hypothetical prote
562	5	3.8	72	2	A00096	probable membrane	635	5	3.8	94	1	W5WLC1	E5 protein - pygmy
563	5	3.8	73	2	C97172	carbon storage reg	636	5	3.8	94	2	I48172	glial fibrillary a
564	5	3.8	74	2	T31047	hypothetical prote	637	5	3.8	94	2	A41492	lik heat shock pro
565	5	3.8	75	2	A00882	probable membrane	638	5	3.8	94	2	F97064	spore coat protein
566	5	3.8	75	2	D61399	hypothetical prote	639	5	3.8	95	2	S66015	ribosomal protein
567	5	3.8	77	1	C58652	adipokinetic hormo	640	5	3.8	95	2	D84327	hypothetical prote
568	5	3.8	77	2	D82819	hypothetical prote	641	5	3.8	95	2	AD0981	conserved hypothet
569	5	3.8	77	2	S1867	ubiquitin-like pro	642	5	3.8	95	2	B82131	conserved hypothet
570	5	3.8	78	2	P00053	hypothetical prote	643	5	3.8	95	2	H69767	hypothetical prote
571	5	3.8	78	2	C83319	conserved hypothet	644	5	3.8	96	2	I68741	integral membrane
572	5	3.8	78	2	T33454	hypothetical prote	645	5	3.8	96	2	AE2331	50S ribosomal prot
573	5	3.8	78	2	S75256	tyrosine-tRNA liga	646	5	3.8	96	2	G81019	chaperonin, 10 kDa
574	5	3.8	79	1	A58656	adipokinetic hormo	647	5	3.8	96	2	G81964	chaperonin 10 kD s
575	5	3.8	79	2	S03266	aspartic proteinas	648	5	3.8	96	2	E69110	hypothetical prote
576	5	3.8	79	2	E83671	hypothetical prote	649	5	3.8	96	2	C64900	outer membrane por
577	5	3.8	79	2	E37204	uncharacterized Zn	650	5	3.8	97	2	AI0538	hypothetical prote
578	5	3.8	80	2	S21770	saposin-C - bovine	651	5	3.8	97	2	T25754	hypothetical prote
579	5	3.8	80	2	G64030	hypothetical prote	652	5	3.8	98	2	A99613	NADH dehydrogenase
580	5	3.8	80	2	T49980	hypothetical prote	653	5	3.8	98	2	T11527	NADH2 dehydrogenas
581	5	3.8	80	2	T48081	hypothetical prote	654	5	3.8	98	2	T11135	NADH2 dehydrogenas
582	5	3.8	81	2	T38451	probable glycoprot	655	5	3.8	98	2	T12887	hypothetical prote
583	5	3.8	81	2	D97617	hypothetical prote	656	5	3.8	99	2	S03525	T-cell receptor al
584	5	3.8	82	2	AB0009	glutaredoxin [limpo	657	5	3.8	99	2	E83235	hypothetical prote
585	5	3.8	83	2	A70768	hypothetical prote	658	5	3.8	99	2	C48653	hypothetical prote
586	5	3.8	83	2	D69153	hypothetical prote	659	5	3.8	100	2	S50333	NADH2 dehydrogenas
587	5	3.8	83	2	T48068	hypothetical prote	660	5	3.8	100	2	S29569	Ig light chain C r
588	5	3.8	83	2	AD1082	B. subtilis Ykud p	661	5	3.8	100	2	AH0077	conserved hypothet
589	5	3.8	83	2	AE1439	B. subtilis Ykud p	662	5	3.8	100	2	G69605	spore coat peptide
590	5	3.8	83	2	AF2544	thioredoxin asl764	663	5	3.8	100	2	F87191	conserved hypothet
591	5	3.8	84	2	AC0027	30S ribosomal prot	664	5	3.8	100	2	T23389	hypothetical prote
592	5	3.8	84	2	T10348	hypothetical prote	665	5	3.8	100	2	C97492	hypothetical prote
593	5	3.8	84	2	E72859	AcOrf-76 protein -	666	5	3.8	100	2	AB2710	conserved hypothet
594	5	3.8	84	2	S36691	hypothetical prote	667	5	3.8	100	2	B98008	hypothetical prote
595	5	3.8	85	1	E64093	ribosomal protein	668	5	3.8	101	2	AC2905	4a-hydroxytetrahyd
596	5	3.8	85	2	A61616	depressant insect	669	5	3.8	101	2	E37476	E4 orf 3' of fiber
597	5	3.8	85	2	I40691	immunity protein 8	670	5	3.8	101	2	E82484	hypothetical prote
598	5	3.8	85	2	T41819	AcWNPV orf76 - Bom	671	5	3.8	101	2	C83047	conserved hypothet
599	5	3.8	86	2	H71510	probable swib (ym7	672	5	3.8	101	2	T25656	hypothetical prote
600	5	3.8	86	2	AB1669	conserved hypothet	673	5	3.8	101	2	AC3161	DNA-invertase [imp
601	5	3.8	87	1	R3NT15	ribosomal protein	674	5	3.8	102	2	E34770	ORF2 protein - sai
602	5	3.8	87	2	E69071	hypothetical prote	675	5	3.8	102	2	F69475	conserved hypothet
603	5	3.8	88	1	R3VM19	ribosomal protein	676	5	3.8	102	2	S65294	probable membrane
604	5	3.8	88	2	S60815	M protein precursor	677	5	3.8	102	2	D72757	hypothetical prote
605	5	3.8	88	2	S68163	SBH2 protein - yea	678	5	3.8	103	2	I50417	RSV-induced protei
606	5	3.8	88	2	AC2561	hypothetical prote	679	5	3.8	103	2	A26736	transformation-ind
607	5	3.8	89	1	S42609	shiga-like toxin -	680	5	3.8	103	2	T49368	hypothetical prote
608	5	3.8	89	2	S58344	shiga-like toxin I	681	5	3.8	103	2	H90234	hypothetical prote
609	5	3.8	89	2	F90779	Shiga toxin 2 subu	682	5	3.8	103	2	S59561	nucleosome assembl
610	5	3.8	89	2	H56640	Shiga toxin 2 subu	683	5	3.8	103	2	D71047	hypothetical prote
611	5	3.8	89	2	A60279	shiga-like toxin I	684	5	3.8	104	2	I47165	cyclolytic trigger
612	5	3.8	89	2	I69156	shiga-like toxin I	685	5	3.8	104	2	E69805	hypothetical prote
613	5	3.8	89	2	S01033	shiga-like toxin I	686	5	3.8	104	2	T49766	hypothetical prote

687	5	3.8	105	2	S36396	H+-transporting tw	760	5	3.8	117	2	T13187	hypothetical prote
688	5	3.8	105	2	T10473	molt-inhibiting ho	761	5	3.8	117	2	T35913	hypothetical prote
689	5	3.8	105	2	D69619	multidrug resistanc	762	5	3.8	117	2	T14283	embryogenic callus
690	5	3.8	105	2	S07742	hypothetical prote	763	5	3.8	117	2	F72468	hypothetical prote
691	5	3.8	105	2	T17281	hypothetical prote	764	-5	3.8	118	2	S21918	T-cell receptor al
692	5	3.8	106	2	C97043	hypothetical prote	765	5	3.8	118	2	S27187	multidrug resistanc
693	5	3.8	107	2	D84391	hypothetical prote	766	5	3.8	118	2	S76608	hypothetical prote
694	5	3.8	107	2	S78532	MTCP-1 protein spl	767	5	3.8	118	2	T07177	probable oleoyl-la
695	5	3.8	107	2	C81420	hypothetical prote	768	5	3.8	118	2	D75065	hypothetical prote
696	5	3.8	107	2	A82642	conserved plasmin	769	5	3.8	118	2	F90459	hypothetical prote
697	5	3.8	107	2	S23472	cpoF protein - Fis	770	5	3.8	118	2	T16510	hypothetical prote
698	5	3.8	107	2	D72487	hypothetical prote	771	5	3.8	118	4	S62173	hypothetical prote
699	5	3.8	107	2	B72494	hypothetical prote	772	5	3.8	119	2	A43635	nitrogenase (EC 1.
700	5	3.8	108	2	A11714	thioredoxin homolo	773	5	3.8	119	2	AB0043	probable cation to
701	5	3.8	108	2	AH1343	thioredoxin homolo	774	5	3.8	119	2	S55161	hypothetical prote
702	5	3.8	108	2	T04117	SEC18 protein homo	775	5	3.8	119	2	H70476	hypothetical prote
703	5	3.8	108	2	T26539	hypothetical prote	776	5	3.8	119	2	A11138	hypothetical prote
704	5	3.8	108	2	B81285	hypothetical prote	777	5	3.8	119	2	C84504	probable CCHC-type
705	5	3.8	108	2	C64455	hypothetical prote	778	5	3.8	119	2	G69112	hypothetical prote
706	5	3.8	108	2	A90116	conserved hypothet	779	5	3.8	119	2	AC1227	hypothetical prote
707	5	3.8	108	2	T21447	hypothetical prote	780	5	3.8	119	2	A86271	F21F23.19 protein
708	5	3.8	109	1	VTHUSE	transforming prote	781	5	3.8	119	2	A71167	hypothetical prote
709	5	3.8	109	2	S27053	thioredoxin - 3mer	782	5	3.8	120	2	C64358	ribosomal protein
710	5	3.8	109	2	T36708	hypothetical prote	783	5	3.8	120	2	F97537	probable glycine c
711	5	3.8	109	2	S41018	hypothetical prote	784	5	3.8	120	2	AG2756	glycine cleavage s
712	5	3.8	109	2	C72685	hypothetical prote	785	5	3.8	120	2	AC0632	membrane protein,
713	5	3.8	109	2	A36757	hypothetical prote	786	5	3.8	120	2	A70799	probable transcrip
714	5	3.8	109	2	C95914	hypothetical heme-	787	5	3.8	120	2	JC2475	growth hormone reg
715	5	3.8	109	2	D87449	conserved hypo/het	788	5	3.8	121	2	S11671	hypothetical prote
716	5	3.8	109	2	T46171	hypothetical prote	789	5	3.8	121	2	B36858	GLI protein - vari
717	5	3.8	110	1	RSBYA1	acidic ribosomal p	790	5	3.8	121	2	T18126	hypothetical prote
718	5	3.8	110	1	R5RTA	ribosomal protein	791	5	3.8	121	2	T40222	hypothetical prote
719	5	3.8	110	1	R5XL32	ribosomal protein	792	5	3.8	122	2	AG2613	conserved hypothet
720	5	3.8	110	2	C71076	hypothetical prote	793	5	3.8	122	2	E97395	hypothetical prote
721	5	3.8	110	2	E71083	hypothetical prote	794	5	3.8	122	2	S57090	hypothetical prote
722	5	3.8	110	2	D82502	hypothetical prote	795	5	3.8	122	2	AB0895	probable exported
723	5	3.8	110	2	A38529	nika protein - Esc	796	5	3.8	122	2	A83756	hypothetical prote
724	5	3.8	110	2	A11860	hypothetical prote	797	5	3.8	122	2	E90948	hypothetical prote
725	5	3.8	111	2	S22899	T-cell receptor al	798	5	3.8	122	2	G64946	lipoprotein yebf p
726	5	3.8	111	2	AG1906	photosystem II pro	799	5	3.8	122	2	A85797	hypothetical prote
727	5	3.8	111	2	H72501	hypothetical prote	800	5	3.8	122	2	F69347	hypothetical prote
728	5	3.8	111	2	T49768	hypothetical prote	801	5	3.8	123	2	S64248	hypothetical prote
729	5	3.8	111	2	T19357	hypothetical prote	802	5	3.8	123	2	B82502	phage shock protei
730	5	3.8	111	2	A83120	ferredoxin [import	803	5	3.8	124	1	T34207	ribosomal protein
731	5	3.8	112	2	E86205	hypothetical prote	804	5	3.8	124	2	S57715	chitinase [EC 3.2.
732	5	3.8	112	2	B96771	protein ribosomal	805	5	3.8	124	2	B70101	holo-acyl-carrier
733	5	3.8	112	2	S73994	hypothetical prote	806	5	3.8	124	2	F95150	crCB protein [impo
734	5	3.8	112	2	T15328	hypothetical prote	807	5	3.8	124	2	D98018	crCB protein [impo
735	5	3.8	112	2	B95380	hypothetical prote	808	5	3.8	124	2	E90804	hypothetical prote
736	5	3.8	113	2	A41830	hypothetical prote	809	5	3.8	124	2	A85613	probable structura
737	5	3.8	113	2	S66967	probable membrane	810	5	3.8	124	2	S08640	hypothetical prote
738	5	3.8	113	2	T48774	hypothetical prote	811	5	3.8	124	2	D70389	hypothetical prote
739	5	3.8	113	2	B41657	probable immunity	812	5	3.8	124	2	T45917	hypothetical prote
740	5	3.8	113	2	C83893	hypothetical prote	813	5	3.8	124	2	T34150	hypothetical prote
741	5	3.8	114	2	A30229	procyelic acidic r	814	5	3.8	124	2	A72464	hypothetical prote
742	5	3.8	114	2	T38286	T cell leukemia/ly	815	5	3.8	124	2	F97745	hypothetical prote
743	5	3.8	114	2	F71925	cag island protein	816	5	3.8	125	2	C83599	conserved hypothet
744	5	3.8	114	2	H64586	cag pathogenicity	817	5	3.8	125	2	A87402	conserved hypothet
745	5	3.8	114	2	C90324	hypothetical prote	818	5	3.8	125	2	D97435	hypothetical prote
746	5	3.8	115	1	FAUTPC	procyelic acidic r	819	5	3.8	126	2	B69989	hypothetical prote
747	5	3.8	115	2	S78279	photosystem II pro	820	5	3.8	126	2	C69776	hypothetical prote
748	5	3.8	115	2	G71058	hypothetical prote	821	5	3.8	126	2	AB2905	conserved hypothet
749	5	3.8	115	2	H72583	hypothetical prote	822	5	3.8	126	2	F83536	probable ring-clea
750	5	3.8	115	2	AE2185	hypothetical prote	823	5	3.8	127	2	A58933	ribosomal protein
751	5	3.8	115	2	D75434	hypothetical prote	824	5	3.8	127	2	S09372	hypothetical prote
752	5	3.8	115	2	AF1366	transcription regu	825	5	3.8	127	2	T43781	hypothetical prote
753	5	3.8	115	2	AG1735	transcription regu	826	5	3.8	127	2	F65098	hypothetical prote
754	5	3.8	115	2	E98167	ferredoxin II [AF2	827	5	3.8	127	2	C91126	hypothetical prote
755	5	3.8	116	2	S07258	helix-destabilizin	828	5	3.8	127	2	B85971	hypothetical prote
756	5	3.8	116	2	D71454	hypothetical prote	829	5	3.8	128	2	S57955	thrombospondin 2 -
757	5	3.8	116	2	C72549	hypothetical prote	830	5	3.8	128	2	F69356	hypothetical prote
758	5	3.8	116	2	B99304	hypothetical prote	831	5	3.8	128	2	A70112	hypothetical prote
759	5	3.8	117	2	G71190	hypothetical prote	832	5	3.8	128	2	S53584	probable membrane

833	5	3.8	128	2	AF1998	hypothetical prote	906	5	3.8	140	1	SXAD95	hexon-associated p
834	5	3.8	129	2	S59126	histone H2A (clone	907	5	3.8	140	2	T03693	ribosomal protein
835	5	3.8	129	2	A26036	procyclic acidic r	908	5	3.8	140	2	F84744	60S ribosomal prot
836	5	3.8	129	2	G90528	hypothetical prote	909	5	3.8	140	2	AH1517	hypothetical prote
837	5	3.8	129	2	H87659	conserved hypotet	910	5	3.8	140	2	T49347	hypothetical prote
838	5	3.8	129	2	F84117	embryonic abundant	911	5	3.8	140	2	E86283	hypothetical prote
839	5	3.8	129	2	G70667	hypothetical prote	912	5	3.8	140	2	I38232	gene SMA3 protein
840	5	3.8	129	2	D82627	hypothetical prote	913	5	3.8	140	2	I38233	gene SMA4 protein
841	5	3.8	130	1	Q7BP77	gene 7.7 protein -	914	5	3.8	140	2	I38234	gene SMA5 protein
842	5	3.8	130	2	A88579	protein T07C4.5 [i	915	5	3.8	141	2	A44438	multidrug drug res
843	5	3.8	130	2	S72926	hypothetical prote	916	5	3.8	141	2	S25272	gene V protein - p
844	5	3.8	130	2	T10347	hypothetical prote	917	5	3.8	141	2	E70916	hypothetical prote
845	5	3.8	130	2	T27438	hypothetical prote	918	5	3.8	141	2	QJ1669	hypothetical 16.1K
846	5	3.8	130	2	S14983	extensin class I (919	5	3.8	141	2	A90130	hypothetical prote
847	5	3.8	130	2	G35905	hypothetical prote	920	5	3.8	142	1	S42721	interleukin-3 prec
848	5	3.8	130	2	G72594	hypothetical prote	921	5	3.8	142	1	S42722	interleukin-3 prec
849	5	3.8	131	2	H86382	hypothetical prote	922	5	3.8	142	2	E90134	40S ribosomal prot
850	5	3.8	131	2	F69103	hypothetical prote	923	5	3.8	142	2	E84040	hypothetical prote
851	5	3.8	131	2	F75117	hypothetical prote	924	5	3.8	142	2	F90015	galactose-6-phosph
852	5	3.8	132	1	E70434	conserved hypotet	925	5	3.8	142	2	A38158	low-temperature re
853	5	3.8	132	2	A44864	fatty acid-binding	926	5	3.8	142	2	QJ2280	hypothetical prote
854	5	3.8	132	2	T29160	hypothetical prote	927	5	3.8	142	2	T51902	hypothetical prote
855	5	3.8	132	2	F42512	G-ORF-A protein -	928	5	3.8	142	2	S70484	RS43 protein - rat
856	5	3.8	132	2	D82278	hypothetical prote	929	5	3.8	142	2	T25879	hypothetical prote
857	5	3.8	132	2	D83003	hypothetical prote	930	5	3.8	143	2	A26918	procyclic acidic r
858	5	3.8	132	2	E72603	hypothetical prote	931	5	3.8	143	2	S59506	ferric pseudobacti
859	5	3.8	132	2	T30595	sugar transport ho	932	5	3.8	143	2	AC1730	hypothetical prote
860	5	3.8	133	1	R3FF49	ribosomal protein	933	5	3.8	143	2	A81251	probable transcrip
861	5	3.8	133	2	S77948	major allergen par	934	5	3.8	144	2	D98172	gamma carboxymuon
862	5	3.8	133	2	A75314	ribosomal protein	935	5	3.8	144	2	AI3114	gamma carboxymuon
863	5	3.8	133	2	T14810	ribosomal protein	936	5	3.8	144	2	AC1907	hypothetical prote
864	5	3.8	133	2	S70967	bifpG protein - Bsc	937	5	3.8	145	2	A44418	procyclin PSSA-1 -
865	5	3.8	133	2	H75296	hypothetical prote	938	5	3.8	145	2	A83010	conserved hypotet
866	5	3.8	133	2	T07205	hypothetical prote	939	5	3.8	145	2	C70328	conserved hypotet
867	5	3.8	133	2	A82955	hypothetical prote	940	5	3.8	145	2	H75108	hypothetical prote
868	5	3.8	133	2	D97680	hypothetical prote	941	5	3.8	145	2	H86517	hypothetical prote
869	5	3.8	133	2	A89917	hypothetical prote	942	5	3.8	145	2	G72103	hypothetical prote
870	5	3.8	133	2	E70334	hypothetical prote	943	5	3.8	145	2	T49888	hypothetical prote
871	5	3.8	133	2	AF2561	hypothetical prote	944	5	3.8	145	2	T06156	hypothetical prote
872	5	3.8	134	1	R3FF32	ribosomal protein	945	5	3.8	145	2	AI1071	DNA polymerase III
873	5	3.8	134	2	A00326	probable membrane	946	5	3.8	145	2	T08000	translation initia
874	5	3.8	134	2	A72754	hypothetical prote	947	5	3.8	146	1	GGNK1B	globin I - ark she
875	5	3.8	134	2	F75170	hypothetical prote	948	5	3.8	146	1	GGNK1D	secretory protein
876	5	3.8	134	2	F69182	conserved hypotet	949	5	3.8	146	2	S70202	secretory protein
877	5	3.8	134	2	C82030	probable cytochrom	950	5	3.8	146	2	E72673	hypothetical prote
878	5	3.8	135	1	RSHU32	ribosomal protein	951	5	3.8	146	2	C86187	hypothetical prote
879	5	3.8	135	1	RSM532	ribosomal protein	952	5	3.8	147	2	S36144	hemoglobin I - ark
880	5	3.8	135	1	RSRT32	ribosomal protein	953	5	3.8	147	2	I46467	luteinizing hormon
881	5	3.8	135	2	I58276	ribosomal protein	954	5	3.8	147	2	D69368	conserved hypotet
882	5	3.8	135	2	S41979	nuclease inhibitor	955	5	3.8	147	2	S67304	probable membrane
883	5	3.8	135	2	A72522	sugar-non-specific	956	5	3.8	147	2	T32403	hypothetical prote
884	5	3.8	135	2	E75616	hypothetical prote	957	5	3.8	147	2	C70312	hypothetical prote
885	5	3.8	135	2	H82834	hypothetical prote	958	5	3.8	147	2	H87607	hypothetical prote
886	5	3.8	135	2	C90527	hypothetical prote	959	5	3.8	148	2	S22088	hypothetical prote
887	5	3.8	135	2	AI0541	probable secreted	960	5	3.8	148	2	D82623	conserved hypotet
888	5	3.8	135	2	B44438	gene ldmr1 protei	961	5	3.8	148	2	F97524	DNAK suppressor pr
889	5	3.8	136	2	G64248	hypothetical prote	962	5	3.8	148	2	S41026	hypothetical prote
890	5	3.8	136	2	S19479	hypothetical prote	963	5	3.8	148	2	E75300	probable membrane
891	5	3.8	136	2	B75086	hypothetical prote	964	5	3.8	148	2	E75300	conserved hypotet
892	5	3.8	136	2	E97847	multidrug resistan	965	5	3.8	148	2	AF1119	PTS system, enzyme
893	5	3.8	137	2	S43885	3-isopropylmalate	966	5	3.8	148	2	AI1479	PTS system, enzyme
894	5	3.8	137	2	D86944	conserved hypotet	967	5	3.8	149	1	R5EC9	ribosomal protein
895	5	3.8	138	1	RSFM29	ribosomal protein	968	5	3.8	149	2	AB1053	50S ribosomal chai
896	5	3.8	138	2	S52933	major allergen par	969	5	3.8	149	2	C86117	50S ribosomal subu
897	5	3.8	138	2	PC2224	peptide LIAE 2 - p	970	5	3.8	149	2	C91276	50S ribosomal subu
898	5	3.8	138	2	S73943	MG076 homolog G07	971	5	3.8	149	2	C82333	ribosomal protein
899	5	3.8	138	2	E84329	hypothetical prote	972	5	3.8	149	2	D64076	ribosomal protein
900	5	3.8	138	2	B87594	proteinase, probab	973	5	3.8	149	2	D83256	heat-shock protein
901	5	3.8	138	2	A96039	degenerate transpo	974	5	3.8	149	2	E90230	partial transposas
902	5	3.8	139	2	T11639	ribosomal protein	975	5	3.8	149	2	T33604	hypothetical prote
903	5	3.8	139	2	AG2743	dnak deletion supp	976	5	3.8	149	2	AF2713	conserved hypotet
904	5	3.8	139	2	T25974	hypothetical prote	977	5	3.8	150	1	E64249	pinin repressor pi
905	5	3.8	140	1	SXAD92	hexon-associated p	978	5	3.8	150	2	AI0429	50S ribosomal prot

979 5 3.8 150 2 C96647 hypothetical prote
980 5 3.8 150 2 G85939 type III secretion
981 5 3.8 150 2 AC0303 hypothetical prote
982 5 3.8 151 1 Q2BPP4 hypothetical prote
983 5 3.8 151 1 S73506 p11B homolog K05_o
984 5 3.8 151 2 D64319 probable format'e d
985 5 3.8 151 2 AC0495 probable acetyltra
986 5 3.8 151 2 T10196 hypothetical prote
987 5 3.8 151 2 S69472 hypothetical prote
988 5 3.8 151 2 B70862 hypothetical prote
989 5 3.8 151 2 E95378 SyzB regulatory pr
990 5 3.8 151 2 S52598 probable membrane
991 5 3.8 151 2 T19087 hypothetical prote
992 5 3.8 151 2 AB3263 thiol/disulfide in
993 5 3.8 152 2 AD0256 probable prophage
994 5 3.8 152 2 H87244 50S ribosomal prot
995 5 3.8 152 2 F90543 conserved hypot'het
996 5 3.8 152 2 F86473 hypothetical prote
997 5 3.8 152 2 T19905 hypothetical prote
998 5 3.8 153 2 JX0072 troponin C, striat
999 5 3.8 153 2 JH0247 guanine nucleotide
1000 5 3.8 153 2 B84036 hypothetical prote

ALIGNMENTS

RESULT 1
S42384
Kruppel-like protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Sep-1997
C:Accession: S42384
R:Smith, A.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42368
A:Accession: S42384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <SM1>
A:Cross-references: EMBL:Z30662; NID:9459581; PID:9459587
C:Genetics:
A:Introns: 10/3; 48/3; 182/3; 315/3; 360/3

Query Match 30.3%; Score 40; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.1e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQKDWGFKFIRDFLLDEANGLLP 119
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Db 134 EETKAMESQRAYRFVQKDWGFKFIRDFLLDEANGLLP 173
|||||

RESULT 2
B64956
flagellar protein flis - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B64956
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B64956
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BLAT>
A:Cross-references: UNIPROT:P26608; GB:AE000285; NID:g1788229; PIDN:AAC74992.
C:Genetics:
A:Gene: flis
C:Superfamily: flagellar protein flis

C:Keywords: flagellum

Query Match 5.3%; Score 7; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 LDEESKD 50
|||||
Db 73 LDEESKD 79

RESULT 3
H90961
flagellar protein Flis [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: H90961
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <HAY>
A:Cross-references: UNIPROT:Q8XBB7; GB:BA000007; PIDN:BA836087.1; PID:g13362132; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs2664
C:Superfamily: flagellar protein flis

Query Match 5.3%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 LDEESKD 50
|||||
Db 73 LDEESKD 79

RESULT 4
H85809
hypothetical protein flis [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85809
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <STO>
A:Cross-references: UNIPROT:Q8XBB7; GB:AE005174; NID:g12516026; PIDN:AAG56940.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: flis
C:Superfamily: flagellar protein flis

Query Match 5.3%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 LDEESKD 50
|||||
Db 73 LDEESKD 79

RESULT 5
A71051

hypothetical protein PH1104 - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
 C:Accession: A71051
 R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: A71051
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-143 <KAW>
 A:Cross-references: UNIPROT:O58831; GB:AP000005; NID:G3236132; PIDN:BA30203.1; PID:G325
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH1104

Query Match 5.3%; Score 7; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 LYLKLV 60
 |||||
 Db 44 LYLKLV 50

RESULT 6
 F82133
 hypothetical protein VC1991 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: F82133
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: F82133
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-145 <HEI>
 A:Cross-references: UNIPROT:Q9KOK7; GB:AE004273; GB:AE003852; NID:G9656517; PIDN:AAF9513
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC1991
 A:Map position: 1

Query Match 5.3%; Score 7; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 FSSGAND 31
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 Db 31 FSSGAND 37

RESULT 7
 JC6050
 homoserine kinase (EC 2.7.1.39) - Lactococcus lactis
 C:Species: Lactococcus lactis
 C>Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
 C:Accession: JC6050
 R:Madsen, S.M.; Albrechtsen, B.; Hansen, E.B.; Israelsen, H.
 J. Bacteriol. 178, 3689-3694, 1996
 A:Title: Cloning and transcriptional analysis of two threonine biosynthetic genes from L
 A:Reference number: JC6049; MUID:96272237; PMID:8682767
 A:Accession: JC6050
 A:Molecule type: mRNA
 A:Residues: 1-296 <MAD>
 A:Cross-references: UNIPROT:P52991; EMBL:X96988; NID:G1255938; PIDN:CAA65714.1; PID:G125

C:Genetics:
 A:Gene: thrB
 C:Function:
 A:Description: catalyzes the conversion of homoserine to threonine
 A:Pathway: threonine biosynthesis
 C:Superfamily: homoserine kinase
 C:Keywords: phosphotransferase; threonine biosynthesis

Query Match 5.3%; Score 7; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 PDDKLT 125
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 Db 259 PDDKLT 265

RESULT 8
 H86769
 homoserine kinase (EC 2.7.1.39) [imported] - Lactococcus lactis subsp. lactis (strain IL
 C:Species: Lactococcus lactis subsp. lactis
 C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C:Accession: H86769
 R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: H86769
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-296 <STO>
 A:Cross-references: UNIPROT:Q9GCD7; GB:AE005176; PID:G12724124; PIDN:AAK05258.1; GSPDB:G
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: thrB
 C:Superfamily: homoserine kinase
 C:Keywords: phosphotransferase

Query Match 5.3%; Score 7; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LLPDDKL 123
 |||||
 Db 257 LLPDDKL 263

RESULT 9
 H95075
 hypothetical protein SP0656 [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: H95075
 R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: H95075
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-302 <KUR>
 A:Cross-references: UNIPROT:Q97RX7; GB:AE005672; PIDN:AAK74801.1; PID:G14972128; GSPDB:G
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP0656

Query Match 5.3%; Score 7; DB 2; Length 302;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 46 EESKDYL 52
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Db 28 EESKDYL 34

RESULT 10
D69744
conserved hypothetical protein ybbI - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: D69744
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
R.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Enian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
A/Authors: Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A/Authors: Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrak, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: D69744
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-304 <KUN>
A/Cross-references: UNIPROT:Q45582; GB:Z99104; GB:AL009126; NID:g26322267; PIDN:CAB11946.
A/Experimental source: strain 168
C/Genetics:
A/Gene: ybbI
C/Superfamily: conserved hypothetical protein b2428

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    Best Local Similarity 100.0%; Pred. No. 24;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 LLEANG 116
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Db 287 LLEANG 293

RESULT 11
C83088
hypothetical protein PA4467 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: C83088
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: C83088
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-310 <STO>
A/Cross-references: UNIPROT:Q9HVU1; GB:AE004860; GB:AE004091; NID:g9950692; PIDN:AAG0785
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA4467

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    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 LDEANGL 117
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Db 195 LDEANGL 201

RESULT 12
A99196
purine nucleosidase, probable (iunH-1) [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: A99196
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan,
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: A99196
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-311 <KUR>
A/Cross-references: UNIPROT:Q97ZS5; GB:AE006641; NID:gl3813662; PIDN:AAK40824.1; GSPDB:GI
C/Genetics:
A/Gene: iunH-1
C/Superfamily: yaaF protein

    Query Match 5.3%; Score 7; DB 2; Length 311;
    Best Local Similarity 100.0%; Pred. No. 25;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 LSLYLL 58
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Db 16 LSLYLL 22

RESULT 13
T45994
hypothetical protein F9D24.250 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T45994
R/D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, January 2000
A/Reference number: Z23011
A/Accession: T45994
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-325 <DAN>
A/Cross-references: UNIPROT:Q9M212; EMBL:AL137081
A/Experimental source: cultivar Columbia; BAC clone F9D24
C/Genetics:
A/Map position: 3
A/Introns: 36/2; 89/1; 198/3
A/Note: F9D24.250
C/Superfamily: Arabidopsis thaliana hypothetical protein F9D24.110

    Query Match 5.3%; Score 7; DB 2; Length 325;
    Best Local Similarity 100.0%; Pred. No. 26;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 DYLSLYL 56
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Db 48 DYLSLYL 54

RESULT 14
G75540
Elac family protein - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: G75540
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F
.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

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A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: G75540
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-331 <WHI>
 A;Cross-references: UNIPROT:Q9RXP0; GB:AE001888; GB:AE000513; NID:g6457936; PIDN:AAF0985
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR0270
 A;Map position: 1
 C;Superfamily: conserved hypothetical protein MJ1502

Query Match 5.3%; Score 7; DB 2; Length 331;
 Best Local Similarity 100.0%; Pred.No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 DFLDEA 114
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 Db 235 DFLDEA 241

RESULT 15

G69474
 conserved hypothetical protein AF1800 - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: G69474
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: G69474
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-340 <KLE>
 A;Cross-references: UNIPROT:Q28474; GB:AE000978; GB:AE000782; NID:g2689301; PIDN:AAB8944

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Qy 53 SLXLLV 59
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 Db 246 SLXLLV 252

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 Job time : 34.8571 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:38:46 ; Search time 24.8286 Seconds
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Title: US-09-706-325-24

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	7	5.3	227	4	US-09-270-767-58283
8	7	5.3	231	4	US-09-134-000C-5641
9	7	5.3	245	4	US-09-393-634-55
10	7	5.3	312	4	US-09-252-991A-24594
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12	7	5.3	430	4	US-09-949-016-10720
13	7	5.3	567	4	US-09-538-092-1365
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17	7	5.3	1068	4	US-09-248-796A-16119
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20	6	4.5	27	2	US-08-436-420-5
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22	6	4.5	33	2	US-08-436-420-3
23	6	4.5	35	2	US-08-436-420-2
24	6	4.5	36	2	US-08-436-420-12
25	6	4.5	39	2	US-08-640-732-8
26	6	4.5	39	5	PCT-US94-12778-8
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28	6	4.5	60	1	US-08-461-859-32
29	6	4.5	60	5	PCT-US93-10069-32
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37	6	4.5	75	4	US-09-213-383-12
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64	6	4.5	156	2	US-09-098-900-4
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66	6	4.5	156	4	US-09-270-767-38302
67	6	4.5	156	4	US-09-270-767-53519
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87	6	4.5	208	3	US-09-280-040-10
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89	6	4.5	208	4	US-09-874-585D-10
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94	6	4.5	214	1	US-08-472-263-3
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Sequence 7133, Ap
Sequence 8309, Ap
Sequence 27049, A
Sequence 25552, A
Sequence 11, Appl
Sequence 17, Appl
Sequence 237, App
Sequence 27894, A
Sequence 20873, A
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Sequence 4508, Ap
Sequence 5689, Ap
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Sequence 7586, Ap
Sequence 3939, Ap
Sequence 4957, Ap
Sequence 3462, Ap
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Sequence 4, Appli
Sequence 38302, A
Sequence 53519, A
Sequence 35784, A
Sequence 51001, A
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Sequence 4582, Ap
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Sequence 5059, Ap
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Sequence 701, App
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Sequence 43542, A
Sequence 15, Appl
Sequence 3883, Ap
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Sequence 33, Appl
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Sequence 22, Appli

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103	6	4.5	229	4	US-09-711-164-447	Sequence 447, App	176	6	4.5	482	4	US-09-538-092-454	Sequence 454, App
104	6	4.5	233	3	US-09-069-023-36	Sequence 36, Appl	177	6	4.5	486	4	US-09-248-796A-20468	Sequence 20468, A
105	6	4.5	234	4	US-09-107-532A-5283	Sequence 5283, Ap	178	6	4.5	494	4	US-09-543-681A-4773	Sequence 4773, Ap
106	6	4.5	237	3	US-08-858-207A-438	Sequence 438, App	179	6	4.5	508	4	US-09-248-796A-19086	Sequence 19086, A
107	6	4.5	240	3	US-09-370-098-5	Sequence 5, Appli	180	6	4.5	521	4	US-09-949-016-11081	Sequence 11081, A
108	6	4.5	242	4	US-09-583-110-435A	Sequence 435A, Ap	181	6	4.5	521	4	US-09-949-016-11082	Sequence 11082, A
109	6	4.5	242	4	US-09-248-796A-14818	Sequence 14818, A	182	6	4.5	521	4	US-09-949-016-11083	Sequence 11083, A
110	6	4.5	246	3	US-09-134-001C-3175	Sequence 3175, Ap	183	6	4.5	539	4	US-09-902-540-11952	Sequence 11952, A
111	6	4.5	257	4	US-09-107-433-3792	Sequence 3792, Ap	184	6	4.5	545	4	US-09-902-540-11418	Sequence 11418, A
112	6	4.5	260	4	US-09-270-767-423A3	Sequence 423A3, A	185	6	4.5	552	4	US-09-543-681A-8131	Sequence 8131, Ap
113	6	4.5	264	1	US-08-188-582-26	Sequence 26, Appl	186	6	4.5	554	4	US-09-252-991A-32632	Sequence 32632, A
114	6	4.5	264	1	US-08-646-715-26	Sequence 26, Appl	187	6	4.5	569	4	US-09-270-767-41817	Sequence 41817, A
115	6	4.5	264	4	US-09-538-092-1355	Sequence 1355, Ap	188	6	4.5	578	4	US-09-252-991A-16850	Sequence 16850, A
116	6	4.5	267	4	US-09-902-540-12826	Sequence 12826, A	189	6	4.5	582	2	US-08-164-292B-29	Sequence 29, Appl
117	6	4.5	268	4	US-09-949-016-10157	Sequence 10157, A	190	6	4.5	582	3	US-08-845-623-29	Sequence 29, Appl
118	6	4.5	271	3	US-09-181-183-36	Sequence 36, Appl	191	6	4.5	582	3	US-08-815-927-29	Sequence 29, Appl
119	6	4.5	271	3	US-09-280-040-36	Sequence 36, Appl	192	6	4.5	582	3	US-09-242-632A-2	Sequence 2, Appli
120	6	4.5	271	3	US-09-277-700-36	Sequence 36, Appl	193	6	4.5	582	3	US-09-103-330-29	Sequence 29, Appl
121	6	4.5	271	4	US-09-874-585D-36	Sequence 36, Appl	194	6	4.5	582	3	US-09-435-242-29	Sequence 29, Appl
122	6	4.5	271	4	US-09-874-585D-53	Sequence 53, Appl	195	6	4.5	584	4	US-09-248-796A-17551	Sequence 17551, A
123	6	4.5	277	4	US-09-438-185A-230	Sequence 230, App	196	6	4.5	608	3	US-08-843-572B-2	Sequence 2, Appli
124	6	4.5	285	2	US-08-712-072C-5	Sequence 5, Appli	197	6	4.5	628	4	US-09-841-786-5	Sequence 5, Appli
125	6	4.5	294	3	US-09-518-046-4	Sequence 4, Appli	198	6	4.5	640	4	US-09-538-092-107	Sequence 107, App
126	6	4.5	294	4	US-09-543-681A-5918	Sequence 5918, Ap	199	6	4.5	643	2	US-08-216-894-8	Sequence 8, Appli
127	6	4.5	295	4	US-09-540-236-2619	Sequence 2619, Ap	200	6	4.5	643	3	US-09-115-746-8	Sequence 8, Appli
128	6	4.5	300	4	US-09-194-146-6	Sequence 6, Appli	201	6	4.5	656	3	US-09-327-984A-36	Sequence 36, Appl
129	6	4.5	300	4	US-09-134-000C-5262	Sequence 5262, Ap	202	6	4.5	661	4	US-09-508-824-8	Sequence 8, Appli
130	6	4.5	307	2	US-08-216-894-6	Sequence 6, Appli	203	6	4.5	691	4	US-09-508-824-9	Sequence 9, Appli
131	6	4.5	307	3	US-09-115-746-6	Sequence 6, Appli	204	6	4.5	699	3	US-09-457-040B-18	Sequence 18, Appl
132	6	4.5	308	2	US-08-695-355-1	Sequence 1, Appli	205	6	4.5	699	4	US-09-902-540-11479	Sequence 11479, A
133	6	4.5	308	2	US-08-695-355-3	Sequence 3, Appli	206	6	4.5	710	4	US-09-252-991A-20733	Sequence 20733, A
134	6	4.5	308	3	US-09-063-869-1	Sequence 3, Appli	207	6	4.5	728	4	US-09-508-824-10	Sequence 10, Appl
135	6	4.5	308	3	US-09-063-869-3	Sequence 3, Appli	208	6	4.5	729	4	US-09-949-016-6544	Sequence 6544, Ap
136	6	4.5	312	4	US-09-902-540-13462	Sequence 13462, A	209	6	4.5	732	4	US-09-438-185A-436	Sequence 436, App
137	6	4.5	322	4	US-09-949-016-8007	Sequence 8007, Ap	210	6	4.5	745	4	US-09-540-236-223A	Sequence 223A, Ap
138	6	4.5	325	4	US-09-252-991A-20421	Sequence 20421, A	211	6	4.5	750	4	US-09-248-796A-14886	Sequence 14886, A
139	6	4.5	326	4	US-09-107-532A-5426	Sequence 5426, Ap	212	6	4.5	775	3	US-09-305-640-2	Sequence 2, Appli
140	6	4.5	327	1	US-08-420-235B-35	Sequence 35, Appl	213	6	4.5	794	4	US-09-949-016-9883	Sequence 9883, Ap
141	6	4.5	327	3	US-08-793-624-35	Sequence 35, Appl	214	6	4.5	799	4	US-09-248-796A-19295	Sequence 19295, A
142	6	4.5	327	4	US-09-248-796A-19580	Sequence 1958, A	215	6	4.5	810	4	US-09-489-039A-9748	Sequence 9748, Ap
143	6	4.5	327	5	PCT-US95-1019A-35	Sequence 35, Appl	216	6	4.5	838	4	US-09-489-039A-9864	Sequence 9864, Ap
144	6	4.5	353	1	US-08-176-620A-14	Sequence 14, Appl	217	6	4.5	849	4	US-09-902-540-15703	Sequence 15703, A
145	6	4.5	353	2	US-08-461-985-14	Sequence 14, Appl	218	6	4.5	875	4	US-09-585-858-18	Sequence 18, Appl
146	6	4.5	353	3	US-08-932-787B-19	Sequence 19, Appl	219	6	4.5	875	4	US-10-270-878-18	Sequence 18, Appl
147	6	4.5	353	3	US-08-932-012C-19	Sequence 19, Appl	220	6	4.5	892	1	US-07-977-434-12	Sequence 12, Appl
148	6	4.5	353	3	US-08-888-818C-19	Sequence 19, Appl	221	6	4.5	892	1	US-08-458-819-12	Sequence 12, Appl
149	6	4.5	355	4	US-09-583-110-3542	Sequence 3542, Ap	222	6	4.5	892	5	PCT-US91-07035-12	Sequence 12, Appl
150	6	4.5	356	4	US-09-107-532A-6286	Sequence 6286, Ap	223	6	4.5	898	4	US-09-252-991A-23689	Sequence 23689, A
151	6	4.5	361	4	US-09-107-433-3933	Sequence 3933, Ap	224	6	4.5	945	4	US-09-198-452A-1030	Sequence 1030, Ap
152	6	4.5	364	4	US-09-205-258-1008	Sequence 1008, Ap	225	6	4.5	946	4	US-09-252-991A-18989	Sequence 18989, A
153	6	4.5	373	4	US-09-252-991A-24545	Sequence 24545, A	226	6	4.5	950	4	US-09-438-185A-959	Sequence 959, App
154	6	4.5	376	4	US-09-543-681A-6740	Sequence 6740, Ap	227	6	4.5	973	2	US-08-683-262B-75	Sequence 75, Appl
155	6	4.5	376	4	US-09-949-016-9185	Sequence 9185, Ap	228	6	4.5	973	3	US-09-361-707-75	Sequence 75, Appl
156	6	4.5	382	4	US-09-134-000C-3829	Sequence 3829, Ap	229	6	4.5	989	4	US-09-540-236-2137	Sequence 2137, Ap
157	6	4.5	383	4	US-09-543-681A-7432	Sequence 7432, Ap	230	6	4.5	998	4	US-09-949-016-8326	Sequence 8326, Ap
158	6	4.5	397	1	US-07-956-697B-5	Sequence 5, Appli	231	6	4.5	1003	1	US-08-571-758-4	Sequence 4, Appli
159	6	4.5	397	1	US-08-263-098-5	Sequence 5, Appli	232	6	4.5	1003	1	US-08-909-984A-4	Sequence 4, Appli
160	6	4.5	400	4	US-09-489-039A-7926	Sequence 7926, Ap	233	6	4.5	1003	1	US-08-909-983-4	Sequence 4, Appli
161	6	4.5	401	4	US-09-252-991A-27198	Sequence 27198, A	234	6	4.5	1036	4	US-10-014-882-2	Sequence 2, Appli
162	6	4.5	422	2	US-08-712-072C-2	Sequence 2, Appli	235	6	4.5	1036	4	US-10-419-279-2	Sequence 2, Appli
163	6	4.5	430	4	US-09-134-000C-5725	Sequence 5725, Ap	236	6	4.5	1093	4	US-09-949-016-11535	Sequence 11535, A
164	6	4.5	436	4	US-09-198-452A-451	Sequence 451, App	237	6	4.5	1093	5	PCT-US93-03077-11	Sequence 11, Appl
165	6	4.5	442	4	US-09-489-039A-11693	Sequence 11693, A	238	6	4.5	1141	1	US-08-363-300-2	Sequence 2, Appli
166	6	4.5	454	3	US-09-518-046-2	Sequence 2, Appli	239	6	4.5	1151	1	US-08-286-889-37	Sequence 37, Appl
167	6	4.5	455	3	US-09-261-416-2	Sequence 2, Appli	240	6	4.5	1151	1	US-08-485-618-37	Sequence 37, Appl
168	6	4.5	455	4	US-08-583-110-3905	Sequence 3905, Ap	241	6	4.5	1151	1	US-08-362-652-37	Sequence 37, Appl
169	6	4.5	458	4	US-08-487-596-16	Sequence 16, Appl	242	6	4.5	1151	2	US-08-605-672-37	Sequence 37, Appl
170	6	4.5	458	4	US-08-484-722-4	Sequence 4, Appli	243	6	4.5	1151	2	US-08-482-293A-37	Sequence 37, Appl
171	6	4.5	458	4	US-08-660-451A-16	Sequence 16, Appl	244	6	4.5	1151	2	US-08-943-363-37	Sequence 37, Appl
172	6	4.5	458	4	US-09-949-016-5986	Sequence 5986, Ap	245	6	4.5	1151	3	US-09-193-043-37	Sequence 37, Appl
173	6	4.5	461	4	US-09-248-796A-16346	Sequence 16346, A	246	6	4.5	1151	4	US-09-688-307A-37	Sequence 37, Appl

247	6	4.5	1151	4	US-09-252-991A-23596	Sequence 23596, A	320	5	3.8	12	4	US-09-403-752A-62	Sequence 62, Appl
248	6	4.5	1151	4	US-09-350-259-37	Sequence 37, Appl	321	5	3.8	12	4	US-09-551-151A-62	Sequence 62, Appl
249	6	4.5	1155	1	US-08-286-889-46	Sequence 46, Appl	322	5	3.8	14	4	US-09-342-325C-64	Sequence 64, Appl
250	6	4.5	1155	1	US-08-485-618-46	Sequence 46, Appl	323	5	3.8	15	2	US-08-428-257A-68	Sequence 68, Appl
251	6	4.5	1155	1	US-08-362-652-46	Sequence 46, Appl	324	5	3.8	16	3	US-08-602-999A-406	Sequence 406, App
252	6	4.5	1155	2	US-08-605-672-46	Sequence 46, Appl	325	5	3.8	16	4	US-09-556-877-39	Sequence 39, Appl
253	6	4.5	1155	2	US-08-482-293A-46	Sequence 46, Appl	326	5	3.8	16	4	US-09-500-124-406	Sequence 406, App
254	6	4.5	1155	2	US-08-943-363-46	Sequence 46, Appl	327	5	3.8	16	4	US-09-288-594A-39	Sequence 39, Appl
255	6	4.5	1155	3	US-09-193-043-46	Sequence 46, Appl	328	5	3.8	16	4	US-09-620-412C-39	Sequence 39, Appl
256	6	4.5	1155	4	US-09-688-307A-46	Sequence 46, Appl	329	5	3.8	16	4	US-09-410-568-39	Sequence 39, Appl
257	6	4.5	1155	4	US-09-350-259-46	Sequence 46, Appl	330	5	3.8	16	4	US-09-598-419-39	Sequence 39, Appl
258	6	4.5	1160	4	US-09-328-352-6826	Sequence 6826, Ap	331	5	3.8	16	4	US-09-920-174-30	Sequence 30, Appl
259	6	4.5	1161	1	US-08-485-618-53	Sequence 53, Appl	332	5	3.8	16	4	US-09-920-195A-30	Sequence 30, Appl
260	6	4.5	1161	1	US-08-485-618-55	Sequence 55, Appl	333	5	3.8	19	2	US-08-318-837-25	Sequence 25, Appl
261	6	4.5	1161	1	US-08-362-652-53	Sequence 53, Appl	334	5	3.8	19	4	US-09-556-877-93	Sequence 93, Appl
262	6	4.5	1161	1	US-08-362-652-55	Sequence 55, Appl	335	5	3.8	19	4	US-09-620-412C-93	Sequence 93, Appl
263	6	4.5	1161	2	US-08-605-672-53	Sequence 53, Appl	336	5	3.8	19	4	US-09-410-568-93	Sequence 93, Appl
264	6	4.5	1161	2	US-08-605-672-55	Sequence 55, Appl	337	5	3.8	19	4	US-09-598-419-93	Sequence 93, Appl
265	6	4.5	1161	2	US-08-482-293A-53	Sequence 53, Appl	338	5	3.8	20	1	US-07-787-148C-1	Sequence 1, Appl
266	6	4.5	1161	2	US-08-482-293A-55	Sequence 55, Appl	339	5	3.8	20	1	US-08-103-742-23	Sequence 23, Appl
267	6	4.5	1161	2	US-08-943-363-53	Sequence 53, Appl	340	5	3.8	20	1	US-08-199-508-19	Sequence 19, Appl
268	6	4.5	1161	2	US-08-943-363-55	Sequence 55, Appl	341	5	3.8	20	1	US-08-199-508-20	Sequence 20, Appl
269	6	4.5	1161	3	US-09-193-043-53	Sequence 53, Appl	342	5	3.8	20	2	US-08-584-972-61	Sequence 61, Appl
270	6	4.5	1161	3	US-09-193-043-55	Sequence 55, Appl	343	5	3.8	20	2	US-08-499-676A-39	Sequence 39, Appl
271	6	4.5	1161	4	US-09-688-307A-53	Sequence 53, Appl	344	5	3.8	20	3	US-09-208-277-13	Sequence 13, Appl
272	6	4.5	1161	4	US-09-350-259-53	Sequence 53, Appl	345	5	3.8	20	4	US-09-556-877-94	Sequence 94, Appl
273	6	4.5	1161	4	US-09-350-259-55	Sequence 55, Appl	346	5	3.8	20	4	US-09-556-877-95	Sequence 95, Appl
274	6	4.5	1161	4	US-09-350-259-55	Sequence 55, Appl	347	5	3.8	20	4	US-09-556-877-98	Sequence 98, Appl
275	6	4.5	1192	4	US-09-902-540-14526	Sequence 14526, A	348	5	3.8	20	4	US-09-556-877-98	Sequence 98, Appl
276	6	4.5	1220	2	US-08-680-346-38	Sequence 38, Appl	349	5	3.8	20	4	US-09-288-594A-13	Sequence 13, Appl
277	6	4.5	1466	4	US-09-262-537-20	Sequence 20, Appl	350	5	3.8	20	4	US-09-620-412C-13	Sequence 13, Appl
278	6	4.5	1337	3	US-08-854-585-2	Sequence 2, Appl	351	5	3.8	20	4	US-09-620-412C-94	Sequence 94, Appl
279	6	4.5	1337	4	US-09-447-533-2	Sequence 2, Appl	352	5	3.8	20	4	US-09-620-412C-95	Sequence 95, Appl
280	6	4.5	1337	5	PCT-US95-05512-2	Sequence 2, Appl	353	5	3.8	20	4	US-09-620-412C-98	Sequence 98, Appl
281	6	4.5	1427	4	US-09-538-092-1044	Sequence 1044, Ap	354	5	3.8	20	4	US-09-410-568-13	Sequence 13, Appl
282	6	4.5	1466	4	US-09-262-537-20	Sequence 20, Appl	355	5	3.8	20	4	US-09-410-568-94	Sequence 94, Appl
283	6	4.5	1466	4	US-09-262-537-58	Sequence 58, Appl	356	5	3.8	20	4	US-09-410-568-95	Sequence 95, Appl
284	6	4.5	1471	4	US-08-811-519-1	Sequence 1, Appl	357	5	3.8	20	4	US-09-410-568-98	Sequence 98, Appl
285	6	4.5	1673	4	US-09-418-710-70	Sequence 70, Appl	358	5	3.8	20	4	US-09-598-419-13	Sequence 13, Appl
286	6	4.5	1673	4	US-09-839-479-69	Sequence 69, Appl	359	5	3.8	20	4	US-09-598-419-94	Sequence 94, Appl
287	6	4.5	1674	4	US-09-418-710-1	Sequence 1, Appl	360	5	3.8	20	4	US-09-598-419-95	Sequence 95, Appl
288	6	4.5	1674	4	US-09-839-479-1	Sequence 1, Appl	361	5	3.8	20	4	US-09-598-419-98	Sequence 98, Appl
289	6	4.5	1706	2	US-08-459-568-2	Sequence 2, Appl	362	5	3.8	20	4	US-09-889-136-5	Sequence 5, Appl
290	6	4.5	1706	2	US-08-399-411-2	Sequence 2, Appl	363	5	3.8	21	2	US-08-194-981E-41	Sequence 41, Appl
291	6	4.5	1706	3	US-08-516-859A-2	Sequence 2, Appl	364	5	3.8	21	2	US-08-499-676A-20	Sequence 20, Appl
292	6	4.5	1706	3	US-09-586-472-2	Sequence 2, Appl	365	5	3.8	21	3	US-08-860-089-2	Sequence 2, Appl
293	6	4.5	1706	4	US-09-528-706-2	Sequence 2, Appl	366	5	3.8	22	1	US-07-755-461A-8	Sequence 8, Appl
294	6	4.5	1724	1	US-08-325-547-3	Sequence 3, Appl	367	5	3.8	22	1	US-08-315-831A-8	Sequence 8, Appl
295	6	4.5	1780	4	US-09-949-016-6899	Sequence 6899, Ap	368	5	3.8	22	2	US-08-662-318-8	Sequence 8, Appl
296	6	4.5	1783	4	US-09-362-336A-2	Sequence 2, Appl	369	5	3.8	22	2	US-08-499-676A-40	Sequence 40, Appl
297	6	4.5	1786	4	US-09-949-016-7880	Sequence 7880, Ap	370	5	3.8	22	4	US-09-549-831-3	Sequence 3, Appl
298	6	4.5	1804	4	US-09-362-336A-4	Sequence 4, Appl	371	5	3.8	22	4	US-08-838-128B-31	Sequence 31, Appl
299	6	4.5	3241	4	US-09-841-786-1	Sequence 1, Appl	372	5	3.8	22	4	US-09-933-999A-14	Sequence 14, Appl
300	5	3.8	5	4	US-09-800-170-53	Sequence 53, Appl	373	5	3.8	22	5	PCT-US95-12509-8	Sequence 8, Appl
301	5	3.8	7	1	US-08-233-788A-49	Sequence 49, Appl	374	5	3.8	23	2	US-08-310-912A-103	Sequence 103, App
302	5	3.8	8	4	US-09-920-174-29	Sequence 29, Appl	375	5	3.8	23	3	US-08-841-089-103	Sequence 103, App
303	5	3.8	8	4	US-09-920-195A-29	Sequence 29, Appl	376	5	3.8	23	3	US-09-301-085-103	Sequence 103, App
304	5	3.8	9	1	US-08-615-181-37	Sequence 37, Appl	377	5	3.8	23	5	PCT-US95-04570-103	Sequence 103, App
305	5	3.8	9	3	US-08-159-339A-631	Sequence 631, App	378	5	3.8	23	5	PCT-US95-04589-103	Sequence 103, App
306	5	3.8	9	3	US-09-518-046-102	Sequence 102, App	379	5	3.8	24	3	US-09-326-039-8	Sequence 8, Appl
307	5	3.8	10	2	US-08-428-257A-44	Sequence 44, Appl	380	5	3.8	26	1	US-07-942-245-295	Sequence 295, App
308	5	3.8	10	3	US-08-405-647B-34	Sequence 34, Appl	381	5	3.8	26	1	US-07-942-245-296	Sequence 296, App
309	5	3.8	10	3	US-08-985-499-34	Sequence 34, Appl	382	5	3.8	26	1	US-07-942-245-333	Sequence 333, App
310	5	3.8	10	4	US-09-305-542A-17	Sequence 17, Appl	383	5	3.8	26	4	US-09-122-144-10	Sequence 10, Appl
311	5	3.8	10	5	PCT-US96-03180-34	Sequence 34, Appl	384	5	3.8	26	4	US-08-838-128B-29	Sequence 29, Appl
312	5	3.8	11	2	US-08-811-897A-3	Sequence 3, Appl	385	5	3.8	27	1	US-08-451-307-25	Sequence 25, Appl
313	5	3.8	11	2	US-08-855-213-3	Sequence 3, Appl	386	5	3.8	27	1	US-08-066-325-82	Sequence 82, Appl
314	5	3.8	11	3	US-09-201-474-3	Sequence 3, Appl	387	5	3.8	27	1	US-08-336-618-1	Sequence 1, Appl
315	5	3.8	11	4	US-09-721-908-16	Sequence 16, Appl	388	5	3.8	28	3	US-09-082-279B-673	Sequence 673, App
316	5	3.8	12	1	US-07-798-776-9	Sequence 9, Appl	389	5	3.8	28	3	US-09-315-304B-673	Sequence 673, App
317	5	3.8	12	3	US-08-251-288A-9	Sequence 9, Appl	390	5	3.8	28	4	US-09-228-900-77	Sequence 77, Appl
318	5	3.8	12	3	US-09-298-819A-9	Sequence 9, Appl	391	5	3.8	28	4	US-09-834-784-673	Sequence 673, App
319	5	3.8	12	3	US-08-860-089-3	Sequence 3, Appl	392	5	3.8	28	4	US-09-442-989-23	Sequence 23, Appl

393	5	3.8	28	4	US-09-515-965A-673	Sequence 673, App	466	5	3.8	35	3	US-09-082-279B-650	Sequence 650, App
394	5	3.8	28	4	US-09-528-200-134	Sequence 134, App	467	5	3.8	35	3	US-09-082-279B-651	Sequence 651, App
395	5	3.8	28	4	US-09-350-641C-673	Sequence 673, App	468	5	3.8	35	3	US-09-082-279B-677	Sequence 677, App
396	5	3.8	28	4	US-09-350-841A-673	Sequence 673, App	469	5	3.8	35	3	US-09-324-455-10	Sequence 10, App1
397	5	3.8	29	1	US-08-218-023-7	Sequence 7, App1	470	5	3.8	35	3	US-08-474-349A-447	Sequence 447, App
398	5	3.8	29	1	US-08-194-981E-39	Sequence 39, App1	471	5	3.8	35	3	US-08-474-349A-448	Sequence 448, App
399	5	3.8	29	2	US-08-194-981E-42	Sequence 42, App1	472	5	3.8	35	3	US-08-474-349A-449	Sequence 449, App
400	5	3.8	29	2	US-08-194-981E-44	Sequence 44, App1	473	5	3.8	35	3	US-08-474-349A-450	Sequence 450, App
401	5	3.8	29	4	US-09-149-476-513	Sequence 513, App	474	5	3.8	35	3	US-08-474-349A-451	Sequence 451, App
402	5	3.8	30	1	US-08-447-411-33	Sequence 33, App1	475	5	3.8	35	3	US-08-474-349A-452	Sequence 452, App
403	5	3.8	30	2	US-08-480-473B-35	Sequence 35, App1	476	5	3.8	35	3	US-08-474-349A-453	Sequence 453, App
404	5	3.8	30	3	US-08-915-213-35	Sequence 35, App1	477	5	3.8	35	3	US-08-474-349A-454	Sequence 454, App
405	5	3.8	30	3	US-09-235-217-35	Sequence 35, App1	478	5	3.8	35	3	US-08-474-349A-455	Sequence 455, App
406	5	3.8	30	4	US-09-402-532-9	Sequence 9, App1	479	5	3.8	35	3	US-08-474-349A-456	Sequence 456, App
407	5	3.8	30	5	PTT-US96-10251-35	Sequence 35, App1	480	5	3.8	35	3	US-08-474-349A-457	Sequence 457, App
408	5	3.8	31	1	US-08-190-802A-254	Sequence 254, App	481	5	3.8	35	3	US-08-474-349A-458	Sequence 458, App
409	5	3.8	31	3	US-08-477-346-254	Sequence 254, App	482	5	3.8	35	3	US-08-474-349A-459	Sequence 459, App
410	5	3.8	31	3	US-08-473-089-254	Sequence 254, App	483	5	3.8	35	3	US-08-474-349A-460	Sequence 460, App
411	5	3.8	31	3	US-09-513-342-22	Sequence 22, App1	484	5	3.8	35	3	US-08-474-349A-461	Sequence 461, App
412	5	3.8	31	4	US-08-487-072A-254	Sequence 254, App	485	5	3.8	35	3	US-08-474-349A-462	Sequence 462, App
413	5	3.8	31	4	US-08-437-943D-102	Sequence 102, App	486	5	3.8	35	3	US-08-474-349A-463	Sequence 463, App
414	5	3.8	31	4	US-08-437-943D-103	Sequence 103, App	487	5	3.8	35	3	US-08-474-349A-464	Sequence 464, App
415	5	3.8	31	4	US-08-437-943D-104	Sequence 104, App	488	5	3.8	35	3	US-09-315-304B-418	Sequence 418, App
416	5	3.8	31	4	US-08-437-943D-105	Sequence 105, App	489	5	3.8	35	3	US-09-315-304B-419	Sequence 419, App
417	5	3.8	31	4	US-08-437-943D-106	Sequence 106, App	490	5	3.8	35	3	US-09-315-304B-420	Sequence 420, App
418	5	3.8	31	4	US-08-437-943D-107	Sequence 107, App	491	5	3.8	35	3	US-09-315-304B-421	Sequence 421, App
419	5	3.8	31	4	US-08-437-943D-108	Sequence 108, App	492	5	3.8	35	3	US-09-315-304B-422	Sequence 422, App
420	5	3.8	31	4	US-08-437-943D-109	Sequence 109, App	493	5	3.8	35	3	US-09-315-304B-423	Sequence 423, App
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423	5	3.8	32	4	US-09-270-767-32021	Sequence 32021, A	496	5	3.8	35	3	US-09-315-304B-426	Sequence 426, App
424	5	3.8	32	4	US-09-270-767-47238	Sequence 47238, A	497	5	3.8	35	3	US-09-315-304B-427	Sequence 427, App
425	5	3.8	33	2	US-08-499-676A-34	Sequence 34, App1	498	5	3.8	35	3	US-09-315-304B-428	Sequence 428, App
426	5	3.8	33	4	US-09-402-532-10	Sequence 10, App1	499	5	3.8	35	3	US-09-315-304B-429	Sequence 429, App
427	5	3.8	34	3	US-09-082-279B-737	Sequence 737, App	500	5	3.8	35	3	US-09-315-304B-430	Sequence 430, App
428	5	3.8	34	3	US-09-315-304B-737	Sequence 737, App	501	5	3.8	35	3	US-09-315-304B-431	Sequence 431, App
429	5	3.8	34	4	US-09-228-990-71	Sequence 71, App1	502	5	3.8	35	3	US-09-315-304B-432	Sequence 432, App
430	5	3.8	34	4	US-08-834-784-737	Sequence 737, App	503	5	3.8	35	3	US-09-315-304B-433	Sequence 433, App
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438	5	3.8	35	3	US-09-014-416-30	Sequence 30, App1	511	5	3.8	35	3	US-09-315-304B-651	Sequence 651, App
439	5	3.8	35	3	US-09-014-416-32	Sequence 32, App1	512	5	3.8	35	3	US-09-315-304B-677	Sequence 677, App
440	5	3.8	35	3	US-09-014-416-34	Sequence 34, App1	513	5	3.8	35	4	US-08-485-546A-210	Sequence 210, App
441	5	3.8	35	3	US-09-014-416-37	Sequence 37, App1	514	5	3.8	35	4	US-08-485-546A-211	Sequence 211, App
442	5	3.8	35	3	US-09-014-416-38	Sequence 38, App1	515	5	3.8	35	4	US-09-834-784-418	Sequence 418, App
443	5	3.8	35	3	US-09-014-416-41	Sequence 41, App1	516	5	3.8	35	4	US-09-834-784-419	Sequence 419, App
444	5	3.8	35	3	US-09-082-279B-418	Sequence 418, App	517	5	3.8	35	4	US-09-834-784-420	Sequence 420, App
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446	5	3.8	35	3	US-09-082-279B-420	Sequence 420, App	519	5	3.8	35	4	US-09-834-784-422	Sequence 422, App
447	5	3.8	35	3	US-09-082-279B-421	Sequence 421, App	520	5	3.8	35	4	US-09-834-784-423	Sequence 423, App
448	5	3.8	35	3	US-09-082-279B-422	Sequence 422, App	521	5	3.8	35	4	US-09-834-784-424	Sequence 424, App
449	5	3.8	35	3	US-09-082-279B-423	Sequence 423, App	522	5	3.8	35	4	US-09-834-784-425	Sequence 425, App
450	5	3.8	35	3	US-09-082-279B-424	Sequence 424, App	523	5	3.8	35	4	US-09-834-784-426	Sequence 426, App
451	5	3.8	35	3	US-09-082-279B-425	Sequence 425, App	524	5	3.8	35	4	US-09-834-784-427	Sequence 427, App
452	5	3.8	35	3	US-09-082-279B-426	Sequence 426, App	525	5	3.8	35	4	US-09-834-784-428	Sequence 428, App
453	5	3.8	35	3	US-09-082-279B-427	Sequence 427, App	526	5	3.8	35	4	US-09-834-784-429	Sequence 429, App
454	5	3.8	35	3	US-09-082-279B-428	Sequence 428, App	527	5	3.8	35	4	US-09-834-784-430	Sequence 430, App
455	5	3.8	35	3	US-09-082-279B-429	Sequence 429, App	528	5	3.8	35	4	US-09-834-784-431	Sequence 431, App
456	5	3.8	35	3	US-09-082-279B-430	Sequence 430, App	529	5	3.8	35	4	US-09-834-784-432	Sequence 432, App
457	5	3.8	35	3	US-09-082-279B-431	Sequence 431, App	530	5	3.8	35	4	US-09-834-784-433	Sequence 433, App
458	5	3.8	35	3	US-09-082-279B-432	Sequence 432, App	531	5	3.8	35	4	US-09-834-784-434	Sequence 434, App
459	5	3.8	35	3	US-09-082-279B-433	Sequence 433, App	532	5	3.8	35	4	US-09-834-784-435	Sequence 435, App
460	5	3.8	35	3	US-09-082-279B-434	Sequence 434, App	533	5	3.8	35	4	US-09-834-784-646	Sequence 646, App
461	5	3.8	35	3	US-09-082-279B-435	Sequence 435, App	534	5	3.8	35	4	US-09-834-784-647	Sequence 647, App
462	5	3.8	35	3	US-09-082-279B-646	Sequence 646, App	535	5	3.8	35	4	US-09-834-784-648	Sequence 648, App
463	5	3.8	35	3	US-09-082-279B-647	Sequence 647, App	536	5	3.8	35	4	US-09-834-784-649	Sequence 649, App
464	5	3.8	35	3	US-09-082-279B-648	Sequence 648, App	537	5	3.8	35	4	US-09-834-784-650	Sequence 650, App
465	5	3.8	35	3	US-09-082-279B-649	Sequence 649, App	538	5	3.8	35	4	US-09-834-784-651	Sequence 651, App

539	5	3.8	35	4	US-09-834-784-677	Sequence 677, App	612	5	3.8	35	4	US-09-350-841A-648	Sequence 648, App
540	5	3.8	35	4	US-09-515-965A-418	Sequence 418, App	613	5	3.8	35	4	US-09-350-841A-649	Sequence 649, App
541	5	3.8	35	4	US-09-515-965A-419	Sequence 419, App	614	5	3.8	35	4	US-09-350-841A-650	Sequence 650, App
542	5	3.8	35	4	US-09-515-965A-420	Sequence 420, App	615	5	3.8	35	4	US-09-350-841A-651	Sequence 651, App
543	5	3.8	35	4	US-09-515-965A-421	Sequence 421, App	616	5	3.8	35	4	US-09-350-841A-677	Sequence 677, App
544	5	3.8	35	4	US-09-515-965A-422	Sequence 422, App	617	5	3.8	35	4	US-09-350-841A-1866	Sequence 1866, App
545	5	3.8	35	4	US-09-515-965A-423	Sequence 423, App	618	5	3.8	35	4	US-10-220-587-12	Sequence 12, App
546	5	3.8	35	4	US-09-515-965A-424	Sequence 424, App	619	5	3.8	36	1	US-08-118-270-242	Sequence 242, App
547	5	3.8	35	4	US-09-515-965A-425	Sequence 425, App	620	5	3.8	36	5	PCT-US93-08528-242	Sequence 242, App
548	5	3.8	35	4	US-09-515-965A-426	Sequence 426, App	621	5	3.8	37	2	US-08-318-837-13	Sequence 13, Appl
549	5	3.8	35	4	US-09-515-965A-427	Sequence 427, App	622	5	3.8	39	3	US-08-860-089-1	Sequence 1, Appl
550	5	3.8	35	4	US-09-515-965A-428	Sequence 428, App	623	5	3.8	39	4	US-08-838-128B-30	Sequence 30, Appl
551	5	3.8	35	4	US-09-515-965A-429	Sequence 429, App	624	5	3.8	41	4	US-09-489-847-220	Sequence 220, App
552	5	3.8	35	4	US-09-515-965A-430	Sequence 430, App	625	5	3.8	41	4	US-09-270-767-40563	Sequence 40563, A
553	5	3.8	35	4	US-09-515-965A-431	Sequence 431, App	626	5	3.8	41	4	US-09-270-767-55779	Sequence 55779, A
554	5	3.8	35	4	US-09-515-965A-432	Sequence 432, App	627	5	3.8	43	3	US-09-082-279B-962	Sequence 962, App
555	5	3.8	35	4	US-09-515-965A-433	Sequence 433, App	628	5	3.8	43	3	US-09-227-357-614	Sequence 614, App
556	5	3.8	35	4	US-09-515-965A-434	Sequence 434, App	629	5	3.8	43	3	US-09-315-304B-962	Sequence 962, App
557	5	3.8	35	4	US-09-515-965A-435	Sequence 435, App	630	5	3.8	43	4	US-09-834-784-962	Sequence 962, App
558	5	3.8	35	4	US-09-515-965A-446	Sequence 446, App	631	5	3.8	43	4	US-09-515-965A-962	Sequence 962, App
559	5	3.8	35	4	US-09-515-965A-647	Sequence 647, App	632	5	3.8	43	4	US-09-350-841C-962	Sequence 962, App
560	5	3.8	35	4	US-09-515-965A-648	Sequence 648, App	633	5	3.8	43	4	US-09-350-841A-962	Sequence 962, App
561	5	3.8	35	4	US-09-515-965A-649	Sequence 649, App	634	5	3.8	44	2	US-08-483-926A-4	Sequence 4, Appl
562	5	3.8	35	4	US-09-515-965A-650	Sequence 650, App	635	5	3.8	44	2	US-08-854-768-4	Sequence 4, Appl
563	5	3.8	35	4	US-09-515-965A-651	Sequence 651, App	636	5	3.8	44	2	US-08-737-045-4	Sequence 4, Appl
564	5	3.8	35	4	US-09-515-965A-677	Sequence 677, App	637	5	3.8	44	3	US-09-053-197A-55	Sequence 55, Appl
565	5	3.8	35	4	US-09-515-965A-1914	Sequence 1914, App	638	5	3.8	44	3	US-09-085-761A-60	Sequence 60, Appl
566	5	3.8	35	4	US-09-350-641C-418	Sequence 418, App	639	5	3.8	44	4	US-09-270-767-39906	Sequence 39906, A
567	5	3.8	35	4	US-09-350-641C-419	Sequence 419, App	640	5	3.8	44	4	US-09-270-767-55123	Sequence 55123, A
568	5	3.8	35	4	US-09-350-641C-420	Sequence 420, App	641	5	3.8	44	4	US-09-471-276-853	Sequence 853, App
569	5	3.8	35	4	US-09-350-641C-421	Sequence 421, App	642	5	3.8	45	3	US-08-486-099-203	Sequence 203, App
570	5	3.8	35	4	US-09-350-641C-422	Sequence 422, App	643	5	3.8	45	3	US-08-484-223B-203	Sequence 203, App
571	5	3.8	35	4	US-09-350-641C-423	Sequence 423, App	644	5	3.8	45	3	US-08-919-597-203	Sequence 203, App
572	5	3.8	35	4	US-09-350-641C-424	Sequence 424, App	645	5	3.8	45	3	US-08-475-668A-203	Sequence 203, App
573	5	3.8	35	4	US-09-350-641C-425	Sequence 425, App	646	5	3.8	45	3	US-08-485-551A-203	Sequence 203, App
574	5	3.8	35	4	US-09-350-641C-426	Sequence 426, App	647	5	3.8	45	3	US-08-471-913A-203	Sequence 203, App
575	5	3.8	35	4	US-09-350-641C-427	Sequence 427, App	648	5	3.8	45	3	US-08-485-264A-203	Sequence 203, App
576	5	3.8	35	4	US-09-350-641C-428	Sequence 428, App	649	5	3.8	45	3	US-09-082-279B-825	Sequence 825, App
577	5	3.8	35	4	US-09-350-641C-429	Sequence 429, App	650	5	3.8	45	3	US-08-474-349A-203	Sequence 203, App
578	5	3.8	35	4	US-09-350-641C-430	Sequence 430, App	651	5	3.8	45	3	US-09-315-304B-825	Sequence 825, App
579	5	3.8	35	4	US-09-350-641C-431	Sequence 431, App	652	5	3.8	45	4	US-08-470-896-203	Sequence 203, App
580	5	3.8	35	4	US-09-350-641C-432	Sequence 432, App	653	5	3.8	45	4	US-08-485-546A-203	Sequence 203, App
581	5	3.8	35	4	US-09-350-641C-433	Sequence 433, App	654	5	3.8	45	4	US-09-834-784-825	Sequence 825, App
582	5	3.8	35	4	US-09-350-641C-434	Sequence 434, App	655	5	3.8	45	4	US-09-515-965A-825	Sequence 825, App
583	5	3.8	35	4	US-09-350-641C-435	Sequence 435, App	656	5	3.8	45	4	US-09-350-641C-825	Sequence 825, App
584	5	3.8	35	4	US-09-350-641C-446	Sequence 446, App	657	5	3.8	45	4	US-09-270-767-57023	Sequence 57023, A
585	5	3.8	35	4	US-09-350-641C-647	Sequence 647, App	658	5	3.8	45	4	US-09-350-841A-825	Sequence 825, App
586	5	3.8	35	4	US-09-350-641C-648	Sequence 648, App	659	5	3.8	46	2	US-08-487-266A-203	Sequence 203, App
587	5	3.8	35	4	US-09-350-641C-649	Sequence 649, App	660	5	3.8	46	2	US-08-480-473B-54	Sequence 54, Appl
588	5	3.8	35	4	US-09-350-641C-650	Sequence 650, App	661	5	3.8	46	2	US-08-511-485-32	Sequence 32, Appl
589	5	3.8	35	4	US-09-350-641C-651	Sequence 651, App	662	5	3.8	46	3	US-08-915-213-54	Sequence 54, Appl
590	5	3.8	35	4	US-09-350-641C-677	Sequence 677, App	663	5	3.8	46	3	US-09-235-217-54	Sequence 54, Appl
591	5	3.8	35	4	US-09-350-641C-1677	Sequence 1677, App	664	5	3.8	46	4	US-09-761-936A-33	Sequence 33, Appl
592	5	3.8	35	4	US-09-350-841A-418	Sequence 418, App	665	5	3.8	46	4	US-09-201-932A-32	Sequence 32, Appl
593	5	3.8	35	4	US-09-350-841A-419	Sequence 419, App	666	5	3.8	46	4	US-09-011-356-32	Sequence 32, Appl
594	5	3.8	35	4	US-09-350-841A-420	Sequence 420, App	667	5	3.8	46	4	US-09-201-932-32	Sequence 32, Appl
595	5	3.8	35	4	US-09-350-841A-421	Sequence 421, App	668	5	3.8	46	4	US-09-270-767-57345	Sequence 57345, A
596	5	3.8	35	4	US-09-350-841A-422	Sequence 422, App	669	5	3.8	47	3	US-09-082-279B-783	Sequence 783, App
597	5	3.8	35	4	US-09-350-841A-423	Sequence 423, App	670	5	3.8	47	3	US-09-315-304B-783	Sequence 783, App
598	5	3.8	35	4	US-09-350-841A-424	Sequence 424, App	671	5	3.8	47	4	US-09-834-784-783	Sequence 783, App
599	5	3.8	35	4	US-09-350-841A-425	Sequence 425, App	672	5	3.8	47	4	US-09-823-266-14	Sequence 14, Appl
600	5	3.8	35	4	US-09-350-841A-426	Sequence 426, App	673	5	3.8	47	4	US-09-515-965A-783	Sequence 783, App
601	5	3.8	35	4	US-09-350-841A-427	Sequence 427, App	674	5	3.8	47	4	US-09-350-841C-783	Sequence 783, App
602	5	3.8	35	4	US-09-350-841A-428	Sequence 428, App	675	5	3.8	47	4	US-08-838-128B-3	Sequence 3, Appl
603	5	3.8	35	4	US-09-350-841A-429	Sequence 429, App	676	5	3.8	47	4	US-09-350-841A-783	Sequence 783, App
604	5	3.8	35	4	US-09-350-841A-430	Sequence 430, App	677	5	3.8	47	4	US-09-471-276-1177	Sequence 1177, App
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607	5	3.8	35	4	US-09-350-841A-433	Sequence 433, App	680	5	3.8	49	3	US-03-082-279B-782	Sequence 782, App
608	5	3.8	35	4	US-09-350-841A-434	Sequence 434, App	681	5	3.8	49	3	US-09-315-304B-782	Sequence 782, App
609	5	3.8	35	4	US-09-350-841A-435	Sequence 435, App	682	5	3.8	49	4	US-09-482-273-180	Sequence 180, App
610	5	3.8	35	4	US-09-350-841A-646	Sequence 646, App	683	5	3.8	49	4	US-09-834-784-782	Sequence 782, App
611	5	3.8	35	4	US-09-350-841A-647	Sequence 647, App	684	5	3.8	49	4	US-09-515-965A-782	Sequence 782, App

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701	5	3.8	51	4	US-08-838-128B-9	Sequence 9, Appli	774	5	3.8	63	4	US-09-543-681A-4455	Sequence 4455, Ap
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847	5	3.8	79	4	US-09-902-540-12742	Sequence 12742, A	920	5	3.8	91	4	Sequence 1514, Ap	
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849	5	3.8	80	1	US-08-225-757B-14	Sequence 14, Appl	922	5	3.8	91	4	Sequence 4943, Ap	
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858	5	3.8	81	4	US-09-482-273-262	Sequence 262, App	931	5	3.8	93	4	Sequence 5079, Ap	
859	5	3.8	81	4	US-09-328-352-6966	Sequence 6966, Ap	932	5	3.8	93	4	Sequence 39835, A	
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874	5	3.8	83	4	US-09-895-752-39	Sequence 39, Appl	947	5	3.8	95	6	Sequence 12, Appl	
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876	5	3.8	83	4	US-09-328-352-7273	Sequence 7273, Ap	949	5	3.8	95	6	Patent No. 5318899	
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878	5	3.8	83	4	US-09-900-787-39	Sequence 39, Appl	951	5	3.8	96	2	Sequence 52, Appl	
879	5	3.8	83	4	US-09-809-665A-119	Sequence 119, App	952	5	3.8	96	2	Sequence 23, Appl	
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882	5	3.8	84	4	US-09-732-210-1459	Sequence 1459, Ap	955	5	3.8	96	2	Sequence 52, Appl	
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884	5	3.8	84	4	US-09-489-039A-8254	Sequence 8254, Ap	957	5	3.8	96	3	Sequence 23, Appl	
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886	5	3.8	85	3	US-09-134-001C-5514	Sequence 5514, Ap	959	5	3.8	96	3	Sequence 23, Appl	
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891	5	3.8	85	4	US-09-599-632-22	Sequence 632, Ap	964	5	3.8	96	4	Sequence 57775, A	
892	5	3.8	86	3	US-09-208-277-5	Sequence 5, Appl	965	5	3.8	96	4	Sequence 16935, A	
893	5	3.8	86	4	US-09-556-877-5	Sequence 5, Appl	966	5	3.8	96	4	Sequence 6718, Ap	
894	5	3.8	86	4	US-09-288-594A-5	Sequence 5, Appl	967	5	3.8	96	4	Sequence 17, Appl	
895	5	3.8	86	4	US-09-620-412C-5	Sequence 5, Appl	968	5	3.8	97	3	Sequence 23, Appl	
896	5	3.8	86	4	US-09-410-568-5	Sequence 5, Appl	969	5	3.8	97	3	Sequence 13, Appl	
897	5	3.8	86	4	US-09-598-419-5	Sequence 5, Appl	970	5	3.8	97	4	Sequence 5794, Ap	
898	5	3.8	86	4	US-09-248-796A-17363	Sequence 17363, A	971	5	3.8	97	4	Sequence 27, Appl	
899	5	3.8	86	4	US-09-513-999C-5434	Sequence 5434, Ap	972	5	3.8	97	4	Sequence 31744, A	
900	5	3.8	86	4	US-09-107-433-2604	Sequence 2604, Ap	973	5	3.8	97	4	Sequence 46961, A	
901	5	3.8	87	4	US-09-732-210-1183	Sequence 1183, Ap	974	5	3.8	97	4	Sequence 60925, A	
902	5	3.8	87	4	US-09-270-767-60167	Sequence 60167, A	975	5	3.8	98	2	Sequence 5, Appl	
903	5	3.8	88	4	US-09-489-087-173	Sequence 173, App	976	5	3.8	98	4	Sequence 4384, Ap	


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977 5 3.8 99 4 US-09-270-767-59996 Sequence 59996, A
978 5 3.8 99 4 US-09-270-767-61780 Sequence 61780, A
979 5 3.8 100 4 US-09-583-110-4600 Sequence 46000, Ap
980 5 3.8 100 4 US-09-270-767-57762 Sequence 57762, A
981 5 3.8 100 4 US-09-710-279-2048 Sequence 2048, Ap
982 5 3.8 100 4 US-09-513-999C-6697 Sequence 6697, Ap
983 5 3.8 100 4 US-09-134-001C-3863 Sequence 3863, Ap
984 5 3.8 101 3 US-09-107-532A-5106 Sequence 5106, Ap
985 5 3.8 101 4 US-09-621-976-4945 Sequence 4945, Ap
986 5 3.8 101 4 US-09-270-767-34998 Sequence 34998, A
987 5 3.8 101 4 US-09-270-767-50215 Sequence 50215, A
988 5 3.8 101 4 US-09-270-767-58656 Sequence 58656, A
989 5 3.8 101 4 US-09-902-540-14311 Sequence 14311, A
990 5 3.8 102 4 US-09-107-532A-5760 Sequence 5760, Ap
991 5 3.8 102 4 US-09-107-532A-6919 Sequence 6919, Ap
992 5 3.8 102 4 US-09-583-110-4874 Sequence 4874, Ap
993 5 3.8 102 4 US-09-270-767-36231 Sequence 36231, A
994 5 3.8 102 4 US-09-270-767-36545 Sequence 36545, A
995 5 3.8 102 4 US-09-270-767-45585 Sequence 45585, A
996 5 3.8 102 4 US-09-270-767-51448 Sequence 51448, A
997 5 3.8 102 4 US-09-270-767-51762 Sequence 51762, A
998 5 3.8 102 4 US-09-270-767-57818 Sequence 57818, A
999 5 3.8 102 4 US-09-949-016-8103 Sequence 8103, Ap
1000 5 3.8 103 3 US-09-134-001C-3738 Sequence 3738, Ap
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ALIGNMENTS

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RESULT 1
US-09-949-016-9724
; Sequence 9724, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9724
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9724
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Query Match 100.0%; Score 132; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.3e-134;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMTINNFSFCREEMGEVKSSTFSSGANDKLWCLRVNPKGLDESKDLSLYLLVLS 60
Db 44 SYMTINNFSFCREEMGEVKSSTFSSGANDKLWCLRVNPKGLDESKDLSLYLLVLS 103

Qy 61 CPKSEVRAKFSLINAKGETKAMESORAYRVQGDWGFKKFIRDFLLDEANGLLP 120
Db 104 CPKSEVRAKFSLINAKGETKAMESORAYRVQGDWGFKKFIRDFLLDEANGLLP 163

Qy 121 DKLTLCFEVSVV 132
Db 164 DKLTLCFEVSVV 175
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RESULT 2
US-09-270-767-42959
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; Sequence 42959, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42959
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42959
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Query Match 30.3%; Score 40; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 8e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 80 EETKAMESQRAYRVQGDWGFKKFIRDFLLDEANGLLP 119
Db 186 EETKAMESQRAYRVQGDWGFKKFIRDFLLDEANGLLP 225
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RESULT 3

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US-08-861-476C-7
; Sequence 7, Application US/08861476C
; Patent No. 6447786
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/08/861,476C
; CURRENT FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-861-476C-7
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Query Match 5.3%; Score 7; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 108 DFLIDEA 114
Db 29 DFLIDEA 35
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RESULT 4

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US-09-519-232-56
; Sequence 56, Application US/09519232
; Patent No. 6528702
; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Tesfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RT2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Brassica napus
US-09-519-232-56
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Query Match 5.3%; Score 7; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 111 LDEANGL 117
| | | | |
Db 21 LDEANGL 27

RESULT 5

US-09-519-232-52
; Sequence 52, Application US/09519232
; Patent No. 6528702

GENERAL INFORMATION:

; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Testaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RTP2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 52
; LENGTH: 166
; TYPE: PRT

; ORGANISM: Brassica napus

US-09-519-232-52

Query Match 5.3%; Score 7; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 LDEANGL 117
| | | | |
Db 21 LDEANGL 27

RESULT 6

US-09-519-232-54
; Sequence 54, Application US/09519232
; Patent No. 6528702

GENERAL INFORMATION:

; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Testaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RTP2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 54
; LENGTH: 166
; TYPE: PRT

; ORGANISM: Brassica napus

US-09-519-232-54

Query Match 5.3%; Score 7; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 LDEANGL 117
| | | | |
Db 21 LDEANGL 27

RESULT 7

US-09-270-767-58283
; Sequence 58283, Application US/09270767
; Patent No. 6703491

; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58283
; LENGTH: 227
; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-58283

Query Match 5.3%; Score 7; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 FCEVSVV 132
| | | | |
Db 11 FCEVSVV 17

RESULT 8

US-09-134-000C-5641
; Sequence 5641, Application US/09134000C
; Patent No. 6617156

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5641
; LENGTH: 231
; TYPE: PRT

; ORGANISM: Enterococcus faecalis

US-09-134-000C-5641

Query Match 5.3%; Score 7; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GLDEESK 49
| | | | |
Db 175 GLDEESK 181

RESULT 9

US-09-393-634-55
; Sequence 55, Application US/09393634
; Patent No. 6558910

GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SP, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 55
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR11
; NAME/KEY: MOD RES
; LOCATION: (1)-(245)
; OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-55

Query Match      5.3%; Score 7; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 LLVSCPK 63
Db 150 LLVSCPK 156

RESULT 10
US-09-252-991A-24594
; Sequence 24594, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24594
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24594

Query Match      5.3%; Score 7; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 LDEANGL 117
Db 197 LDEANGL 203

RESULT 11
US-09-949-016-6081
; Sequence 6081, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6081
; LENGTH: 419
; TYPE: PRT

; ORGANISM: Human
US-09-949-016-6081

Query Match      5.3%; Score 7; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 FSILNAK 78
Db 41 FSILNAK 47

RESULT 12
US-09-949-016-10720
; Sequence 10720, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10720
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10720

Query Match      5.3%; Score 7; DB 4; Length 430;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 FSILNAK 78
Db 51 FSILNAK 57

RESULT 13
US-09-538-092-1365
; Sequence 1365, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormer Version 0.9
; SEQ ID NO 1365
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q92696
US-09-538-092-1365
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Query Match      5.3%; Score 7; DB 4; Length 567;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 CLRVNPK 42
Db 99 CLRVNPK 105

RESULT 14
US-09-583-110-5255
; Sequence 5255, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583.110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5255
; LENGTH: 684
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5255

Query Match      5.3%; Score 7; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 BESKDYL 52
Db 410 BESKDYL 416

RESULT 15
US-09-107-433-4260
; Sequence 4260, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS
; AND THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
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; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 691 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...691
; SEQUENCE DESCRIPTION: SEQ ID NO: 4260:
US-09-107-433-4260

Query Match      5.3%; Score 7; DB 4; Length 691;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 BESKDYL 52
Db 417 BESKDYL 423

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:37:15 ; Search time 99.45 Seconds
(without alignments)
787.814 Million cell updates/sec

Title: US-09-706-325-12

Perfect score: 153

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	153	100.0	979	2	Q94972
5	124	81.0	928	2	Q8CHC5
6	124	81.0	961	2	Q6PCX9
7	79	51.6	721	2	Q95LW3
8	9	5.9	508	1	G101.HUMAN
9	8	5.2	210	2	Q349T7
10	8	5.2	286	2	Q65003
11	8	5.2	423	2	Q63CU1
12	8	5.2	435	2	Q81S14
13	8	5.2	435	2	Q6HK87
14	8	5.2	1045	2	Q8E8P3
15	7	4.6	98	2	Q89T67
16	7	4.6	124	2	Q52117
17	7	4.6	174	2	Q7P7W8
18	7	4.6	198	2	Q46025
19	7	4.6	198	2	Q6NGT3
20	7	4.6	233	2	Q7UJ29
21	7	4.6	246	2	Q82FC0
22	7	4.6	253	2	Q9XAL5
23	7	4.6	255	2	Q74D44
24	7	4.6	257	2	Q9WXV4
25	7	4.6	261	2	Q70EC9
26	7	4.6	271	2	Q6REK7
27	7	4.6	278	2	Q7UEF2
28	7	4.6	280	2	Q8NQ59
29	7	4.6	285	2	Q9UZA2
30	7	4.6	307	2	Q87TD8
31	7	4.6	316	2	Q9XWH8

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34	7	4.6	320	2	Q98K82
35	7	4.6	320	2	Q81N26
36	7	4.6	320	2	Q6HG72
37	7	4.6	321	2	Q813B9
38	7	4.6	325	2	Q8BRB6
39	7	4.6	330	2	Q92N54
40	7	4.6	339	2	Q889P7
41	7	4.6	355	2	Q8R831
42	7	4.6	357	2	Q8NUC9
43	7	4.6	366	2	Q6A7R5
44	7	4.6	369	2	Q8G211
45	7	4.6	377	2	Q8YFW9
46	7	4.6	430	2	Q61PL4
47	7	4.6	433	2	Q7QBX7
48	7	4.6	441	2	Q9V792
49	7	4.6	444	2	Q86823
50	7	4.6	454	2	Q6CGZ2
51	7	4.6	493	2	Q6VUB6
52	7	4.6	496	2	Q8ERP3
53	7	4.6	504	2	Q6RJO6
54	7	4.6	505	2	Q61UV3
55	7	4.6	505	2	Q631B3
56	7	4.6	505	2	Q72X18
57	7	4.6	505	2	Q815C6
58	7	4.6	505	2	Q81K57
59	7	4.6	505	2	Q8ET62
60	7	4.6	505	2	Q6HB48
61	7	4.6	507	2	Q929S7
62	7	4.6	507	2	Q71X82
63	7	4.6	507	2	Q9X4A5
64	7	4.6	509	2	Q7RX54
65	7	4.6	510	2	Q62RF3
66	7	4.6	510	2	Q7NQ38
67	7	4.6	512	1	OPUD_BACSU
68	7	4.6	512	2	Q65FZ6
69	7	4.6	525	2	Q6VTH4
70	7	4.6	546	2	Q8CP33
71	7	4.6	548	2	Q7X226
72	7	4.6	548	2	Q931S4
73	7	4.6	548	2	Q99UC9
74	7	4.6	548	2	Q7A0Z0
75	7	4.6	548	2	Q6G9L0
76	7	4.6	548	2	Q6GH56
77	7	4.6	553	2	Q7PWV8
78	7	4.6	555	2	Q8BH92
79	7	4.6	555	2	Q8C3C6
80	7	4.6	555	2	Q8C3W8
81	7	4.6	579	2	Q6PBG3
82	7	4.6	586	2	Q6ZPW4
83	7	4.6	617	2	Q64M08
84	7	4.6	620	2	Q813X9
85	7	4.6	633	2	Q753Y3
86	7	4.6	633	2	Q755J3
87	7	4.6	651	2	Q9H4F0
88	7	4.6	651	2	Q9NYV6
89	7	4.6	702	2	Q7MW63
90	7	4.6	705	2	Q7R282
91	7	4.6	727	2	Q9X119
92	7	4.6	769	2	Q6Z0U0
93	7	4.6	795	2	Q7ZVP1
94	7	4.6	801	2	Q7MZU4
95	7	4.6	818	2	Q9SLI6
96	7	4.6	851	2	Q7UHJ3
97	7	4.6	890	2	Q7XUD5
98	7	4.6	904	2	Q48541
99	7	4.6	905	2	Q9FYI0
100	7	4.6	944	2	Q8IK09
101	7	4.6	962	2	Q9S7S8
102	7	4.6	1014	2	Q68JA2
103	7	4.6	1014	2	Q7WUD4
104	7	4.6	1044	2	Q70CT4

Q7t2h3 oncorhynchu
Q8kjc1 rhizobium l
Q98k82 rhizobium l
Q81n26 bacillus an
Q6hg72 bacillus th
Q813b9 bacillus ce
Q8brb6 mus musculu
Q92n54 rhizobium m
Q889p7 pseudomonas
Q8r831 thermoanaer
Q8nuc9 corynebacte
Q6a7r5 propionibac
Q8g211 brucella me
Q8yfw9 brucella me
Q6ipl4 homo sapien
Q7qbx7 anopheles g
Q9v792 streptophila
Q86823 streptomyce
Q6cgr2 yarrowia li
Q6vub6 marinococcu
Q8erp3 oceanobacil
Q8rjq6 halobacillu
Q6iuv3 halobacillu
Q631b3 bacillus ce
Q72x18 bacillus ce
Q815c6 bacillus ce
Q81k57 bacillus an
Q8et62 oceanobacil
Q6hb48 bacillus th
Q929s7 listeria in
Q71x82 listeria mo
Q9x4a5 listeria mo
Q7rx54 neurospora
Q8zrf3 bacillus li
Q7nq38 chromobacte
P5417 bacillus su
Q65fz6 bacillus li
Q6vth4 marinococcu
Q8cp33 staphylococ
Q7x226 staphylococ
Q931s4 staphylococ
Q99uc9 staphylococ
Q7a0z0 staphylococ
Q6g9l0 staphylococ
Q6gh56 staphylococ
Q7pwv8 anopheles g
Q8bh92 m mus muscu
Q8c3c6 mus musculu
Q8c3w8 mus musculu
Q6ppg3 chlamydomon
Q8zpw4 mus musculu
Q84m8 bacteroides
Q813x9 bacillus ce
Q753y3 ashbya goss
Q755j3 ashbya goss
Q9h4f0 homo sapien
Q9nyv6 homo sapien
Q7mv63 porphyronom
Q7r282 giardia lam
Q9x119 arabidopsis
Q6z0u0 oryza sativ
Q7zvp1 brachydanio
Q7mzu4 photorhabdu
Q9sl16 arabidopsis
Q7uhj3 rhodopirell
Q7xud5 oryza sativ
Q48541 hordeum vul
Q9fyi0 hordeum vul
Q8ik09 plasmodium
Q9s7s8 hordeum vul
Q68ja2 escherichia
Q7wud4 escherichia
Q70ct4 arabidopsis

105	7	4.6	1052	2	Q7UUB8	Q7uub8 rhodopi-rel
106	7	4.6	1165	2	Q81341	Q81341 plasmodium
107	7	4.6	1351	2	Q8XZ58	Q8xz58 raistonia s
108	7	4.6	1369	2	Q6NZJ7	Q6nzj7 mus musculus
109	7	4.6	1390	2	Q8TH66	Q8th66 dictyosteli
110	7	4.6	1515	2	Q96VK4	Q96vk4 emericella
111	7	4.6	1777	2	Q89278	Q89278 himetobi p
112	7	4.6	1777	2	Q8F3H3	Q8f3h3 himetobi p
113	7	4.6	2224	2	Q8P8Y4	Q8p8y4 xanthomonas
114	7	4.6	3805	2	Q7Y1L1	Q7y1l1 cryptospori
115	7	4.6	4578	2	Q42181	Q42181 fugu rubrip
116	7	4.6	13536	2	Q83VS0	Q83vs0 pseudomonas
117	6	3.9	31	2	Q76030	Q76030 homo sapien
118	6	3.9	38	2	Q7R6R2	Q7r6r2 giardia lam
119	6	3.9	38	2	Q44102	Q44102 rattus norv
120	6	3.9	40	2	Q33162	Q33162 methanosa
121	6	3.9	44	2	Q06684	Q06684 treponema d
122	6	3.9	47	2	Q73198	Q73198 wolbachia p
123	6	3.9	50	2	Q6VE09	Q6veq9 mycobacteri
124	6	3.9	54	2	Q75QM5	Q75qm5 bacterioph
125	6	3.9	54	2	Q7Q6K7	Q7q6k7 borrelia ga
126	6	3.9	56	2	Q70BF8	Q70bf8 bacterioph
127	6	3.9	58	2	Q6KAW2	Q6kaw2 pneumocvsti
128	6	3.9	61	2	Q72763	Q72763 homo sapien
129	6	3.9	61	2	Q7F6K8	Q7f6k8 borrelia ga
130	6	3.9	62	2	Q7Y3G0	Q7y3g0 streptococ
131	6	3.9	62	2	Q8ETG1	Q8etg1 borrelia ga
132	6	3.9	64	2	Q7R130	Q7r130 plasmodium
133	6	3.9	64	2	Q41403	Q41403 sesbania ro
134	6	3.9	65	2	Q9F6C5	Q9f6c5 borrelia ga
135	6	3.9	65	2	Q41019	Q41019 paramecium
136	6	3.9	66	2	Q6RUP9	Q6rup9 homo sapien
137	6	3.9	71	2	Q96W62	Q96w62 pneumocvsti
138	6	3.9	71	2	Q96W63	Q96w63 pneumocvsti
139	6	3.9	71	2	Q96W64	Q96w64 pneumocvsti
140	6	3.9	71	2	Q96W65	Q96w65 pneumocvsti
141	6	3.9	71	2	Q96W66	Q96w66 pneumocvsti
142	6	3.9	71	2	Q96W67	Q96w67 pneumocvsti
143	6	3.9	77	2	Q97W40	Q97w40 sulfolobus
144	6	3.9	79	2	Q9P935	Q9p935 clonostachy
145	6	3.9	80	2	Q6Z1J5	Q6z1j5 oryza sativ
146	6	3.9	81	2	Q9XGV1	Q9xgv1 lycopersico
147	6	3.9	83	2	Q7MJA7	Q7mja7 vibrio vuln
148	6	3.9	83	2	Q7MNE2	Q7mb2 vibrio vuln
149	6	3.9	84	2	Q67186	Q67186 oryza sativ
150	6	3.9	85	2	Q7RM06	Q7rm06 plasmodium
151	6	3.9	85	2	Q9XHG3	Q9xhg3 arabidopsis
152	6	3.9	86	2	Q49969	Q49969 solanum tub
153	6	3.9	86	2	Q6VER6	Q6ver6 mycobacteri
154	6	3.9	86	2	Q9F6K6	Q9f6k6 borrelia ga
155	6	3.9	87	2	Q6PBH7	Q6pbh7 brachydanio
156	6	3.9	89	2	Q911T3	Q911t3 pseudomonas
157	6	3.9	90	2	Q709R9	Q709r9 human immun
158	6	3.9	94	2	Q9RJN0	Q9rjn0 streptomyce
159	6	3.9	97	2	Q87GH3	Q87gh3 vibrio para
160	6	3.9	97	2	Q8E3A3	Q8e3a3 streptococ
161	6	3.9	98	2	Q24186	Q24186 oryza sativ
162	6	3.9	98	2	Q8H317	Q8h317 oryza sativ
163	6	3.9	98	2	Q6AQ57	Q6aq57 desulfotale
164	6	3.9	101	2	Q49968	Q49968 solanum tub
165	6	3.9	101	2	Q81UH7	Q81uh7 bacillus an
166	6	3.9	102	1	RS10_TREDE	Q73pn2 treponema d
167	6	3.9	102	1	RS10_TREPA	Q83218 treponema p
168	6	3.9	102	2	Q14278	Q14278 homo sapien
169	6	3.9	102	2	Q811X0	Q811x0 plasmodium
170	6	3.9	105	2	Q6MY55	Q6mys5 aspergillus
171	6	3.9	105	2	Q6AP72	Q6ap72 desulfotale
172	6	3.9	106	2	Q89S46	Q89s46 bradyrhizob
173	6	3.9	108	2	Q63FB0	Q63fb0 bacillus ce
174	6	3.9	108	2	Q73CT3	Q73ct3 bacillus ce
175	6	3.9	108	2	Q6HMT4	Q6hmt4 bacillus th
176	6	3.9	109	2	Q6YXJ4	Q6yxj4 oryza sativ
177	6	3.9	109	2	Q81HB7	Q81hb7 bacillus ce

Q9arx7	oryza sativ
Q97612	sulfolobus
Q6nc40	rhodopseudo
Q7qla1	anopheles g
P90861	caenorhabdi
Q989A4	vicia faba
P76196	escherichia
Q654K8	oryza sativ
Q7uuh2	shigella fl
Q80117	petromyzon
Q6n539	rhodopseudo
Q8bt4	mus musculu
Q7qzb7	giardia lam
Q94es4	pisum sativ
Q729Y5	desulfovibr
Q9w218	drosofila
Q6aah7	propionibac
Q6d2Q0	erwinia car
Q86u47	homo sapien
Q86030	chlamydia s
O06566	mycobacteri
Q7u0m4	mycobacteri
Q6mdm6	parachlamyd
Q8tm09	methanosa
Q83kv9	shigella fl
Q8rh45	escherichia
Q8x5y6	escherichia
Q929D4	listeria in
Q82nh2	streptomyce
Q8bjx7	mus musculu
Q29186	archaeoglob
Q7mm63	vibrio vuln
Q7na2	vibrio para
Q8d8A5	vibrio vuln
Q9acy7	streptomyce
Q8q0T6	methanosa
Q8y535	listeria mo
Q71xc4	listeria mo
Q82193	streptomyce
Q89bq1	bradyrhizob
O67011	aquifex aeo
Q91t36	arabidopsis
Q7pin0	anopheles g
Q9fc41	streptomyce
Q9xfid2	oryza sativ
O54938	ondatra zib
Q94es3	pisum sativ
Q729e0	desulfovibr
Q61z33	methanococ
Q9y244	homo sapien
Q7qzpb	giardia lam
Q9cxv8	mus musculu
Q9cz17	mus musculu
Q9cqt5	m mus muscu
Q8pt42	methanosa
Q87ud6	oryza sativ
Q8kg57	chlorobium
Q67625	meleagrid h
Q6zqg0	homo sapien
Q08439	saccharomyc
Q8abf9	bacteroides
Q8knp6	bacillus th
Q68v63	uncultured
Q68v64	uncultured
Q68v66	uncultured
Q68v67	uncultured
Q68v68	uncultured
Q68v72	uncultured
Q68v73	uncultured
Q68v74	uncultured
Q68v79	uncultured
Q68v80	uncultured
Q93nf3	arthrobacte

AQUAE

251	6	3.9	147	2	Q2M26	Q92m26 rhizobium m	324	6	3.9	188	2	O30134	O30134 archaeoglob
252	6	3.9	147	2	Q37P5	Q737p5 bacillus ce	325	6	3.9	188	2	P73277	P73277 synechocyst
253	6	3.9	148	2	Q22500	Q22500 caenorhabdi	326	6	3.9	188	2	O9JL38	O9JL38 mus musculus
254	6	3.9	149	1	Y281_LEIXX	Q6ah32 leifsonia x	327	6	3.9	189	2	O74323	O74323 e signal pe
255	6	3.9	149	2	Q89012	Q89012 lactobacilli	328	6	3.9	189	2	O8A356	O8A356 bacteroides
256	6	3.9	150	2	Q66086	Q66086 canine herp	329	6	3.9	189	2	Q9PCH8	Q9PCH8 xyella fas
257	6	3.9	152	2	Q9MFC5	Q9mfc5 beta vulgar	330	6	3.9	190	1	CYGB_HUMAN	CYGB_HUMAN
258	6	3.9	153	2	Q64A10	Q64a10 uncultured	331	6	3.9	190	2	Q8N2X5	Q8N2X5 homo sapien
259	6	3.9	153	2	Q8YJQ9	Q8YjQ9 brucella me	332	6	3.9	190	2	Q8GHN3	Q8GHN3 pseudomonas
260	6	3.9	154	2	Q7M127	Q7m127 daucus caro	333	6	3.9	191	1	PTH_MYCBO	PTH_MYCBO
261	6	3.9	154	2	Q7XZ67	Q7xz67 griffithsia	334	6	3.9	191	1	PTH_MYCTU	PTH_MYCTU
262	6	3.9	155	2	Q7VP20	Q7vp20 haemophilus	335	6	3.9	191	2	Q741V9	Q741V9 mycobacteri
263	6	3.9	157	2	Q8DXN3	Q8dxn3 streptococc	336	6	3.9	191	2	YN42_CAUCR	YN42_CAUCR
264	6	3.9	158	2	Q8XQL8	Q8xql8 ralsstonia s	337	6	3.9	193	2	Q9NX89	Q9NX89 homo sapien
265	6	3.9	158	2	Q7VL01	Q7vl01 haemophilus	338	6	3.9	194	2	Q66080	Q66080 canine herp
266	6	3.9	159	2	Q73640	Q73640 synechocyst	339	6	3.9	195	2	Q9NAJ1	Q9NAJ1 caenorhabdi
267	6	3.9	160	2	Q7N1H1	Q7n1h1 photorhabdu	340	6	3.9	196	2	Q9VAA1	Q9VAA1 drosophila
268	6	3.9	161	1	RUI1_METWA	Q8PY53 methanosarc	341	6	3.9	196	2	Q6FDU6	Q6FDU6 acinetobact
269	6	3.9	161	2	Q8U414	Q8u414 pyrococcus	342	6	3.9	196	2	Q83D18	Q83D18 coxiella bu
270	6	3.9	161	2	Q9HB69	Q9hb69 homo sapien	343	6	3.9	197	2	Q9VZ32	Q9VZ32 drosophila
271	6	3.9	161	2	Q32085	Q32085 bacillus su	344	6	3.9	198	2	Q7RYR1	Q7RYR1 neurospora
272	6	3.9	161	2	Q7ME07	Q7me07 vibrio vuln	345	6	3.9	198	2	Q6YV95	Q6YV95 oryza sativ
273	6	3.9	161	2	Q7WE75	Q7we75 bordetella	346	6	3.9	199	1	PTH_MYCLE	PTH_MYCLE
274	6	3.9	161	2	Q6S9W2	Q6s9w2 columbid ci	347	6	3.9	199	2	Q6EN01	Q6EN01 trimeresuru
275	6	3.9	162	2	Q64EG2	Q64eg2 uncultured	348	6	3.9	199	2	Q8PA66	Q8PA66 xanthomonas
276	6	3.9	162	2	Q87Z67	Q87z67 pseudomonas	349	6	3.9	200	2	Q9PX32	Q9PX32 human herpe
277	6	3.9	164	2	Q05127	Q05127 neisseria g	350	6	3.9	200	2	Q9W8K2	Q9W8K2 human herpe
278	6	3.9	165	2	Q98LE9	Q98le9 rhizobium l	351	6	3.9	200	2	Q9YUA9	Q9YUA9 human immun
279	6	3.9	165	2	Q747H7	Q747h7 geobacter s	352	6	3.9	201	2	Q7QNV9	Q7QNV9 giardia lam
280	6	3.9	166	2	Q6XND3	Q6xnd3 rhodococcus	353	6	3.9	201	2	Q7YXH2	Q7YXH2 caenorhabdi
281	6	3.9	171	1	YCBV_ECOLI	P75860 escherichia	354	6	3.9	202	2	Q6VOK5	Q6VOK5 mycobacteri
282	6	3.9	171	2	Q8PHF9	Q8phf9 xanthomonas	355	6	3.9	203	2	Q9KMZ7	Q9KMZ7 vibrio chol
283	6	3.9	171	2	Q82N41	Q82n41 streptomyce	356	6	3.9	204	2	Q9RC46	Q9RC46 bacillus ha
284	6	3.9	172	2	Q87CK2	Q87ck2 xylella fas	357	6	3.9	204	2	Q98HN0	Q98HN0 rhizobium l
285	6	3.9	172	2	Q312Q0	Q312q0 pseudomonas	358	6	3.9	205	2	Q8ID59	Q8ID59 plasmodium
286	6	3.9	175	2	Q84R71	Q84r71 oryza sativ	359	6	3.9	205	2	Q9HZD9	Q9HZD9 pseudomonas
287	6	3.9	177	2	Q8IRP2	Q8irp2 drosophila	360	6	3.9	206	1	YX59_PSESM	YX59_PSESM
288	6	3.9	178	2	Q82Y10	Q82y10 pyrobaculum	361	6	3.9	206	2	Q74N80	Q74N80 nanoarchaeu
289	6	3.9	178	2	Q97051	Q97051 pseudocardi	362	6	3.9	206	2	Q7PIX6	Q7PIX6 anopheles g
290	6	3.9	178	2	Q87568	Q87568 helicobacte	363	6	3.9	206	2	Q86EJ3	Q86EJ3 schistosoma
291	6	3.9	178	2	Q8CR33	Q8cr33 staphylococ	364	6	3.9	206	2	Q8BRQ1	Q8BRQ1 mus musculu
292	6	3.9	178	2	Q9A5S1	Q9a5s1 caulobacter	365	6	3.9	208	1	Y4B5_PSEPK	Y4B5_PSEPK
293	6	3.9	179	2	Q7QIN0	Q7qin0 anopheles g	366	6	3.9	208	2	Q8H014	Q8H014 oryza sativ
294	6	3.9	179	2	Q8KW25	Q8kw25 ruigeria sp	367	6	3.9	208	2	O8YHJ5	O8YHJ5 brucella me
295	6	3.9	179	2	Q87VNO	Q87vn0 pseudomonas	368	6	3.9	209	1	GEMI_HUMAN	GEMI_HUMAN
296	6	3.9	179	2	Q88HE4	Q88he4 pseudomonas	369	6	3.9	211	2	Q8BSI3	Q8BSI3 mus musculu
297	6	3.9	179	2	Q9QUC6	Q9quc6 tt virus..o	370	6	3.9	212	2	Q9C9K9	Q9C9K9 arabidopsis
298	6	3.9	180	2	Q50971	Q50971 neisseria g	371	6	3.9	212	2	O85372	O85372 rhodococcus
299	6	3.9	180	2	Q8G0B3	Q8g0b3 brucella su	372	6	3.9	212	2	O83VI0	O83VI0 corynobacte
300	6	3.9	181	2	Q74KA6	Q74ka6 lactobacilli	373	6	3.9	213	2	O65EP8	O65ef8 bacillus li
301	6	3.9	181	2	Q7DD77	Q7dd77 neisseria m	374	6	3.9	213	2	Q7UMS1	Q7umel rhodopirell
302	6	3.9	181	2	Q9JQK6	Q9jqk6 neisseria m	375	6	3.9	214	2	Q7QM4	Q7qm4 anopheles g
303	6	3.9	182	2	Q04410	Q04410 raphanus sa	376	6	3.9	214	2	Q657Y6	Q657Y6 oryza sativ
304	6	3.9	182	2	Q6RV21	Q6rv21 bifidobacte	377	6	3.9	215	1	RPB5_CANGA	RPB5_CANGA
305	6	3.9	182	2	Q8DXJ9	Q8dxj9 synechococc	378	6	3.9	215	1	RPB5_YEAST	RPB5_YEAST
306	6	3.9	183	1	DIN1_RAPSA	P27626 raphanus sa	379	6	3.9	215	2	Q9XEX0	Q9xex0 gracillaria
307	6	3.9	183	2	Q21131	Q21131 caenorhabdi	380	6	3.9	215	2	O8X4F4	O8X4e4 escherichia
308	6	3.9	183	2	Q9HXU2	Q9hxu2 pseudomonas	381	6	3.9	217	2	Q72A59	Q72a59 desulfovibr
309	6	3.9	184	2	Q8JF87	Q8jf87 human immun	382	6	3.9	218	1	YD12_MYCPN	YD12_MYCPN
310	6	3.9	185	2	Q9A357	Q9a357 bacteroides	383	6	3.9	218	2	Q75A56	Q75A56 ashbya goes
311	6	3.9	186	1	RRF_RHOA	Q7uth0 rhodopirell	384	6	3.9	219	2	Q9AS64	Q9AS64 oryza sativ
312	6	3.9	186	1	TNR5_PSEAE	P06691 pseudomonas	385	6	3.9	222	2	Q75AR6	Q75ar6 ashbya goes
313	6	3.9	186	1	TNR7_ECOLI	P06692 escherichia	386	6	3.9	222	2	Q7WGT6	Q7wgt6 bordetella
314	6	3.9	186	2	O66046	O66046 pseudomonas	387	6	3.9	223	2	Q972K5	Q972k5 sulfolobus
315	6	3.9	186	2	Q934S3	Q934s3 thioabacillu	388	6	3.9	223	2	Q64RB3	Q64rb3 bacteroides
316	6	3.9	186	2	Q68E60	Q68e60 aeromonas p	389	6	3.9	223	2	Q7VTZ4	Q7vtz4 bordetella
317	6	3.9	186	2	Q7AXT9	Q7axt9 pseudomonas	390	6	3.9	223	2	Q7WK92	Q7wk92 bordetella
318	6	3.9	186	2	Q7BE17	Q7be17 shigella fl	391	6	3.9	224	2	Q82M30	Q82m30 streptomyce
319	6	3.9	186	2	Q9AJD0	Q9ajd0 pseudomonas	392	6	3.9	224	2	Q9RU88	Q9ru88 deinococcus
320	6	3.9	186	2	Q65IT1	Q65it1 bacillus li	393	6	3.9	225	2	Q9ZBV3	Q9zbv3 streptomyce
321	6	3.9	187	2	Q7AG38	Q7ag38 escherichia	394	6	3.9	226	2	Q9C828	Q9c828 arabidopsis
322	6	3.9	187	2	Q8X581	Q8x581 escherichia	395	6	3.9	226	2	O33188	O33188 mycobacteri
323	6	3.9	187	2	Q83RX8	Q83rx8 shigella fl	396	6	3.9	226	2	Q7TZS6	Q7tzs6 mycobacteri

397	6	3.9	227	2	Q6C587	Q6c587 yarrowia li
398	6	3.9	227	2	Q7MUR2	Q7mur2 porphyromon
399	6	3.9	227	2	Q9RWX2	Q9rxw2 deinococcus
400	6	3.9	230	1	AQP2_PSEPK	Q88f17 pseudomonas
401	6	3.9	230	1	U1L16_HCMVA	U1l657 human cytom
402	6	3.9	230	2	Q8H6C0	Q8h6c0 silene lati
403	6	3.9	230	2	Q7M6R7	Q7m6r7 human cytom
404	6	3.9	230	2	Q7TF85	Q7tf85 human cytom
405	6	3.9	231	2	Q67SV4	Q67sv4 symbiobacte
406	6	3.9	232	2	Q9LAS2	Q9las2 desulfitoba
407	6	3.9	232	2	Q8ZNO9	Q8zn09 salmonella
408	6	3.9	232	2	Q74I11	Q74i11 lactobacill
409	6	3.9	233	2	Q787Z8	Q787z8 pneumocysti
410	6	3.9	233	2	Q78730	Q78730 pneumocysti
411	6	3.9	233	2	Q6TLZ5	Q6tlz5 mycobacteri
412	6	3.9	233	2	Q9Z240	Q9z240 rhizobium m
413	6	3.9	233	2	Q7JNGN2	Q7jngn2 gloeobacter
414	6	3.9	233	2	Q9JV64	Q9jv64 neisseria m
415	6	3.9	233	2	Q3K054	Q3k054 neisseria m
416	6	3.9	234	1	SNG1_HUMAN	Q43759 homo sapien
417	6	3.9	234	1	SNG1_MOUSE	Q51000 mus musculu
418	6	3.9	234	1	SNG1_RAT	Q62876 rattus norv
419	6	3.9	234	2	Q26747	Q26747 methanobact
420	6	3.9	235	2	Q662E2	Q662e2 borrelia ga
421	6	3.9	235	2	Q92KY7	Q92ky7 rhizobium m
422	6	3.9	236	2	Q8ZWR9	Q8zwr9 pyrobaculum
423	6	3.9	236	2	Q8ZB22	Q8zb22 enterococcu
424	6	3.9	239	2	Q987U4	Q987u4 rhizobium l
425	6	3.9	239	2	Q8D2M8	Q8d2m8 wiggleswort
426	6	3.9	239	2	Q9KFK5	Q9kfk5 bacillus ha
427	6	3.9	240	2	Q30144	Q30144 archaeoglob
428	6	3.9	240	2	Q6NCCT7	Q6ncc7 rhodopseudo
429	6	3.9	241	2	Q6FPW6	Q6fpw6 candida gla
430	6	3.9	242	2	Q81JV6	Q81jv6 plasmod.um
431	6	3.9	242	2	Q7Z0H0	Q7z0h0 plasmod.um
432	6	3.9	242	2	Q82RL6	Q82rl6 streptomyce
433	6	3.9	242	2	Q6AKI2	Q6aki2 desulfotale
434	6	3.9	242	2	Q8BF77	Q8bf77 uncultured
435	6	3.9	242	2	Q6RXJ0	Q6rxj0 human cytom
436	6	3.9	242	2	Q75RX5	Q75rx5 oreochromis
437	6	3.9	243	2	Q6INE4	Q6ine4 xenopus lae
438	6	3.9	244	2	Q8WQV9	Q8wqv9 aphroca.lis
439	6	3.9	244	2	Q74K22	Q74k22 lactobacill
440	6	3.9	245	2	Q8Y1B9	Q8y1b9 ralstonia s
441	6	3.9	245	2	Q88I43	Q88i43 pseudomonas
442	6	3.9	246	2	Q6IWO4	Q6iww4 burkholderi
443	6	3.9	246	2	Q9SY37	Q9sy37 arabidopsis
444	6	3.9	246	2	Q8RGR2	Q8rgb2 fusobacteri
445	6	3.9	246	2	Q6NGD2	Q6ngd2 corynebacte
446	6	3.9	246	2	Q7NFW3	Q7nfv3 gloeobacter
447	6	3.9	247	1	Y125_RICPR	P41087 rickettsia
448	6	3.9	247	1	Y167_RICCN	Q92ja0 rickettsia
449	6	3.9	247	2	Q7PAR7	Q7par7 rickettsia
450	6	3.9	247	2	Q8PPL6	Q8ppl6 xanthomonas
451	6	3.9	247	2	Q68XP2	Q68xp2 rickettsia
452	6	3.9	247	2	Q9KFL0	Q9kfl0 bacillus ha
453	6	3.9	247	2	Q8BF96	Q8bf96 uncultured
454	6	3.9	248	1	GRPE_ANASP	P95438 pseudomonas
455	6	3.9	248	2	Q73ECO	Q73eco bacillus ce
456	6	3.9	248	2	Q9I314	Q9i314 pseudomonas
457	6	3.9	249	2	Q6D4P3	Q6d4p3 erwinia car
458	6	3.9	249	2	Q8UJ80	Q8uj80 agrobacteri
459	6	3.9	250	2	Q9LTG7	Q9ltg7 arabidopsis
460	6	3.9	250	2	Q636V7	Q636v7 bacillus ce
461	6	3.9	250	2	Q8YMY8	Q8ymv8 anabaena sp
462	6	3.9	250	2	Q733B4	Q733b4 bacillus ce
463	6	3.9	250	2	Q81AG9	Q81ag9 bacillus ce
464	6	3.9	250	2	Q81W66	Q81w66 bacillus an
465	6	3.9	250	2	Q6HF92	Q6hf92 bacillus th
466	6	3.9	251	2	Q663S0	Q663s0 yersinia ps
467	6	3.9	251	2	Q829T6	Q829t6 yersinia pe
468	6	3.9	251	2	Q7P501	Q7p501 fusobacteri
469	6	3.9	252	2		

470	6	3.9	252	2	Q8RH62	Q8rh62 fusobacteri
471	6	3.9	253	2	Q97YU2	Q97yu2 sulfolobus
472	6	3.9	253	2	Q70MM8	Q70mm8 crassostrea
473	6	3.9	254	2	Q9UF65	Q9uf65 homo sapien
474	6	3.9	255	2	Q78727	Q78727 pneumocysti
475	6	3.9	255	2	Q6NLM6	Q6nlm6 drosophila
476	6	3.9	255	2	Q68049	Q68049 rhodobacter
477	6	3.9	255	2	Q88NR7	Q88nr7 pseudomonas
478	6	3.9	256	2	Q9S209	Q9s209 trypanosoma
479	6	3.9	256	2	Q7PE56	Q7pe56 anopheles g
480	6	3.9	256	2	Q9DXV5	Q9dxv5 tomato spot
481	6	3.9	257	1	DLHH_SULSO	P95862 sulfolobus
482	6	3.9	258	2	Q8FY43	Q8fy43 brucella su
483	6	3.9	259	2	Q92KZ5	Q92kz5 rhizobium m
484	6	3.9	260	2	Q6BQC2	Q6bqc2 debaryomyce
485	6	3.9	260	2	Q7VM79	Q7vm79 haemophilus
486	6	3.9	261	2	Q96XK4	Q96xk4 sulfolobus
487	6	3.9	261	2	Q78729	Q78729 pneumocysti
488	6	3.9	261	2	Q94YM6	Q94ym6 rana nigrom
489	6	3.9	261	2	Q6L7I1	Q6l7i1 buergeria b
490	6	3.9	262	2	Q98CP4	Q98cp4 rhizobium l
491	6	3.9	261	2	Q7VSJ8	Q7vsj8 bordetella
492	6	3.9	261	2	Q7W459	Q7w459 bordetella
493	6	3.9	261	2	Q7WFL6	Q7wfl6 bordetella
494	6	3.9	262	2	Q9RB26	Q9rb26 peptobacter
495	6	3.9	262	2	Q9XB51	Q9xb51 erwinia car
496	6	3.9	262	2	Q6CZM8	Q6czm8 erwinia car
497	6	3.9	263	2	Q6NJH0	Q6njh0 corynebacte
498	6	3.9	264	2	Q87202	Q87202 azospirillu
499	6	3.9	264	2	Q9HZV7	Q9hzv7 pseudomonas
500	6	3.9	265	2	Q7QQF8	Q7qqf8 giardia lam
501	6	3.9	265	2	Q8RPD5	Q8rpd5 legionella
502	6	3.9	265	2	Q9FDK8	Q9fdk8 zymomonas m
503	6	3.9	265	2	Q7V3Z4	Q7v3z4 prochloroco
504	6	3.9	266	2	Q7VNX0	Q7vnx0 haemophilus
505	6	3.9	266	2	Q6DCS4	Q6dcs4 brachydanio
506	6	3.9	267	2	Q6CLX9	Q6clx9 kluyveromyc
507	6	3.9	268	1	ET1B_XENLA	P18756 xenopus lae
508	6	3.9	268	2	Q8I6J7	Q8i6j7 ciona intes
509	6	3.9	269	2	Q9W4X7	Q9w4x7 drosophila
510	6	3.9	269	2	Q74PA9	Q74pa9 yersinia pe
511	6	3.9	269	2	Q8YBG1	Q8ybg1 brucella me
512	6	3.9	269	2	Q89FH2	Q89fh2 bradyrhizob
513	6	3.9	269	2	Q8CFZ9	Q8cfz9 yersinia pe
514	6	3.9	269	2	Q8FWY4	Q8fwy4 brucella su
515	6	3.9	270	2	Q74DN6	Q74dn6 geobacter s
516	6	3.9	271	2	P78731	P78731 pneumocysti
517	6	3.9	272	2	Q97L38	Q97l38 clostridium
518	6	3.9	273	2	Q91G96	Q91g96 columbid ci
519	6	3.9	273	2	Q91GA1	Q91ga1 columbid ci
520	6	3.9	273	2	Q91G42	Q91g42 columbid ci
521	6	3.9	274	1	GADX_ECO27	P58230 escherichia
522	6	3.9	274	1	GADX_ECO57	P58230 escherichia
523	6	3.9	274	1	GADX_ECOL6	P58230 escherichia
524	6	3.9	274	1	GADX_ECOLI	P37639 escherichia
525	6	3.9	274	1	GADX_SHIFL	Q83pr0 shigella fl
526	6	3.9	274	1	THCF_RHOER	Q05691 rhodococcus
527	6	3.9	275	2	Q9A3U3	Q9a3u3 caulobacter
528	6	3.9	275	2	Q9CCW0	Q9ccw0 mycobacteri
529	6	3.9	275	2	Q6Z9X5	Q6z9x5 oryza sativ
530	6	3.9	276	2	Q737L6	Q737l6 bacillus ce
531	6	3.9	276	2	Q86ZC6	Q86zc6 gibberella
532	6	3.9	277	2	Q53640	Q53640 streptococc
533	6	3.9	277	2	Q88YF6	Q88yf6 pseudomonas
534	6	3.9	277	2	Q8DYF6	Q8dyf6 streptococc
535	6	3.9	277	2	Q8DZN3	Q8dzn3 streptococc
536	6	3.9	277	2	Q8FPY2	Q8fpy2 corynebacte
537	6	3.9	278	1	BMRR_BACSU	P39075 bacillus su
538	6	3.9	278	2	Q64773	Q64773 arabidopsis
539	6	3.9	278	2	Q40768	Q40768 prunus dulc
540	6	3.9	280	2	Q8PI45	Q8pi45 xanthomonas
541	6	3.9	280	2	Q64NUI	Q64nul bacteroides
542	6	3.9	281	2		

543	6	3.9	282	2	Q8TJZ1	Q8Tjz1 methanosaarc	616
544	6	3.9	282	2	Q74B06	Q74bq6 geobacter s	617
545	6	3.9	283	1	X781 YEAST	P47148 saccharomyc	618
546	6	3.9	283	2	Q9AA26	Q9aa26 caulobacter	619
547	6	3.9	285	2	Q97UF4	Q97uf4 sulfolobus	620
548	6	3.9	286	2	Q53710	Q53710 mycobacteri	621
549	6	3.9	286	2	Q7U252	Q7u252 mycobacteri	622
550	6	3.9	286	2	Q9K706	Q9k7q6 bacillus ha	623
551	6	3.9	287	2	Q6TMV7	Q6tmv7 hyphomonas	624
552	6	3.9	287	2	Q8PNR7	Q8pnb7 xanthomonas	625
553	6	3.9	287	2	Q9CHQ9	Q9chq9 lactococcus	626
554	6	3.9	287	2	Q6DFS0	Q6dfs0 xenopus tro	627
555	6	3.9	288	2	Q6CVR6	Q6cvc6 kluyveromyc	628
556	6	3.9	288	2	Q9XU24	Q9xuz4 caenorhabdi	629
557	6	3.9	289	2	Q8YU11	Q8yul1 abaena ep	630
558	6	3.9	289	2	Q9J5R0	Q9j5e0 fowlpox vir	631
559	6	3.9	290	1	EXOS_BPT5	P06229 bacterioph	632
560	6	3.9	291	1	Y620 METJA	Q58037 methanococ	633
561	6	3.9	291	2	Q97I16	Q97i16 clostridium	634
562	6	3.9	292	1	MDCB ACICA	Q9gm3 acinetobact	635
563	6	3.9	292	2	Q8LAG0	Q8lag0 arabidopsis	636
564	6	3.9	292	2	Q9FW11	Q9fwt1 arabidopsis	637
565	6	3.9	292	2	Q9FY94	Q9fy94 arabidopsis	638
566	6	3.9	293	1	YFIE ECOLI	Q33634 escherichia	639
567	6	3.9	293	2	Q72JW2	Q72jw2 thermus the	640
568	6	3.9	294	2	Q94E53	Q94e53 oryza sativ	641
569	6	3.9	294	2	Q9FW23	Q9fw23 arabidopsis	642
570	6	3.9	294	2	Q8P7C3	Q8p7c3 xanthomonas	643
571	6	3.9	295	2	Q8PIP6	Q8pip6 xanthomonas	644
572	6	3.9	295	2	Q20811	Q20811 caenorhabdi	645
573	6	3.9	295	2	Q8PAE8	Q8pae8 xanthomonas	646
574	6	3.9	296	1	MALG_ECOLI	P68185 escherichia	647
575	6	3.9	296	1	MALG_ECOL6	P68184 escherichia	648
576	6	3.9	296	1	MALG_ENTAB	P68183 escherichia	649
577	6	3.9	296	1	MALG_PHOII	P18814 enterobacte	650
578	6	3.9	296	1	MALG_SALTI	Q7n983 photorhabdu	651
579	6	3.9	296	1	MALG_SALTY	Q8zlu3 salmonella	652
580	6	3.9	296	1	MALG_SHIFL	P36468 salmonella	653
581	6	3.9	296	1	Q6CD51	P68186 shigella fl	654
582	6	3.9	296	2	Q664X1	Q6cd51 yarrowia li	655
583	6	3.9	297	2	Q7VIG3	Q664x1 yersinia ps	656
584	6	3.9	297	2	Q9A589	Q7vig3 helicobacte	657
585	6	3.9	297	2	Q9HX00	Q9a589 caulobacter	658
586	6	3.9	297	2	Q8QXV0	Q8hx00 pseudomonas	659
587	6	3.9	297	2	Q8QXV0	Q8qxy0 garlic late	660
588	6	3.9	297	2	Q8UZA2	Q8uza2 garlic late	661
589	6	3.9	298	2	Q8X121	Q8x121 pneumocysti	662
590	6	3.9	299	2	Q9ZMX6	Q8zmx6 salmonella	663
591	6	3.9	299	2	Q7MR96	Q7mr96 wolinnella s	664
592	6	3.9	300	2	Q9VDJ3	Q9vdj3 drosophila	665
593	6	3.9	300	2	Q7D9X3	Q7d9x3 mycobacteri	666
594	6	3.9	300	2	P96811	P96811 mycobacteri	667
595	6	3.9	300	2	Q6ARY6	Q6ary6 desulfotale	668
596	6	3.9	300	2	Q9E7N7	Q9e7n7 lettuce nec	669
597	6	3.9	301	2	Q26437	Q26437 methanobact	670
598	6	3.9	301	2	Q65HT3	Q6sh73 bacillus li	671
599	6	3.9	301	2	Q9PPG1	Q9ppg1 bradyrhizob	672
600	6	3.9	303	1	MALG_YERPE	Q4arf8 yersinia pe	673
601	6	3.9	303	2	Q6EUG3	Q6eug3 oryza sativ	674
602	6	3.9	303	2	Q8PLN1	Q8pln1 xanthomonas	675
603	6	3.9	303	2	Q9K3X6	Q9k3x6 streptomyc	676
604	6	3.9	303	2	Q7ZZ63	Q7zz63 brachydanio	677
605	6	3.9	304	1	ASPA_PROMM	Q7v516 prochloroco	678
606	6	3.9	304	2	Q9BKX6	Q9bkx6 caenorhabdi	679
607	6	3.9	304	2	Q8EIN6	Q8ein6 shewanelia	680
608	6	3.9	305	1	FMT_CAMJE	Q8pi28 campylobact	681
609	6	3.9	305	2	P72579	P72579 sulfolobus	682
610	6	3.9	305	2	Q96Y68	Q96y68 lactococcus	683
611	6	3.9	305	2	Q32796	Q32796 lactococcus	684
612	6	3.9	305	2	Q32798	Q32798 lactococcus	685
613	6	3.9	305	2	Q7ND98	Q7nd98 gloeobacter	686
614	6	3.9	305	2	Q835V5	Q835v5 enterococcu	687
615	6	3.9	305	2	Q9L259	Q9l259 streptomyc	688

P06599	daucus caro	306	1	EXTN DAUCA	P06599 daucus caro
P32311	saccharomyc	307	1	YMC1 YEAST	P32311 saccharomyc
Q61gc7	brachydanio	307	2	Q61OC7	Q61gc7 brachydanio
Q8ffl2	escherichia	308	2	Q8FFL2	Q8ffl2 escherichia
Q83q11	shigella fl	308	2	Q83Q11	Q83q11 shigella fl
Q8x5a8	escherichia	308	2	Q8X5A8	Q8x5a8 escherichia
Q96ej8	homo sapien	309	2	Q96EJ8	Q96ej8 homo sapien
Q86x20	homo sapien	309	2	Q86X20	Q86x20 homo sapien
Q7mp27	vibrio vuln	309	2	Q7MP27	Q7mp27 vibrio vuln
Q7n0a8	photorhabdu	309	2	Q7N0A8	Q7n0a8 photorhabdu
P16925	tetrathymena	310	1	CNJC_TETTH	P16925 tetrathymena
P96562	amycolotops	310	2	P96562	P96562 amycolotops
Q44984	caenorhabdi	311	2	O44984	Q44984 caenorhabdi
Q87un8	pseudomonas	311	2	Q87UM8	Q87un8 pseudomonas
Q26631	methanobact	312	1	Y531 METTH	Q26631 methanobact
Q8y7l1	listeria mo	312	2	Q8Y7L1	Q8y7l1 listeria mo
Q720f6	listeria mo	312	2	Q720F6	Q720f6 listeria mo
Q89588	clostridium	312	2	Q895S8	Q89588 clostridium
Q6cln0	kluyveromyc	313	2	O6CLN0	Q6cln0 kluyveromyc
Q25523	helicobacte	313	2	O25523	Q25523 helicobacte
Q8y556	listeria mo	313	2	Q8Y556	Q8y556 listeria mo
Q71xe5	listeria mo	313	2	Q71XE5	Q71xe5 listeria mo
Q9ka02	bacillus ha	313	2	Q9KA02	Q9ka02 bacillus ha
Q8zkz4	helicobacte	313	2	Q8ZKZ4	Q8zkz4 helicobacte
Q8yjb0	brucella me	314	1	HEM3 BRUME	Q8yjb0 brucella me
Q8fy16	brucella su	314	1	HEM3_BRUSU	Q8fy16 brucella su
Q6e298	arabidopsis	315	2	O6E298	Q6e298 arabidopsis
Q9fx92	arabidopsis	315	2	Q9FX92	Q9fx92 arabidopsis
Q8cna0	staphylococ	315	2	Q8CNA0	Q8cna0 staphylococ
Q58654	pyrococcus	316	2	O58654	Q58654 pyrococcus
Q65vx4	mannheimia	316	2	O65VX4	Q65vx4 mannheimia
Q88i21	pseudomonas	316	2	Q88I21	Q88i21 pseudomonas
Q9pn61	campylobact	316	2	Q9PN61	Q9pn61 campylobact
Q738b3	basillus ce	317	2	Q738B3	Q738b3 basillus ce
Q87m7	oryza sativ	318	2	Q7R9B3	Q87m7 oryza sativ
Q9rht5	streptomyc	318	2	Q9RHT5	Q9rht5 streptomyc
Q82chl	streptomyc	318	2	Q82CH1	Q82chl streptomyc
Q89xk4	bradyrhizob	318	2	Q89XK4	Q89xk4 bradyrhizob
Q8kvd3	vibrio chol	318	2	Q8KVD3	Q8kvd3 vibrio chol
Q9pm73	campylobact	319	2	Q9PM73	Q9pm73 campylobact
Q8s629	oryza sativ	319	2	O8S629	Q8s629 oryza sativ
Q83x38	streptomyc	319	2	Q83X38	Q83x38 streptomyc
Q7mt26	porphyromon	319	2	Q7MT26	Q7mt26 porphyromon
Q8c187	mus musculu	319	2	O8C187	Q8c187 mus musculu
Q66996	basillus su	320	2	O66996	Q66996 basillus su
Q97gf5	clostridium	320	2	Q97GF5	Q97gf5 clostridium
Q73m86	treponema d	320	2	Q73M86	Q73m86 treponema d
Q67qa9	syndromia d	321	2	Q67QA9	Q67qa9 syndromia d
Q986m3	rhizobium l	321	2	Q986M3	Q986m3 rhizobium l
Q83i0	mus musculu	321	2	Q83I0	Q83i0 mus musculu
Q883c4	rhizobium l	322	2	Q883C4	Q883c4 rhizobium l
Q8jfw6	brachydanio	322	2	Q8JFW6	Q8jfw6 brachydanio
Q6kzu0	picophilius	322	2	O6KZU0	Q6kzu0 picophilius
Q650s2	bacteroides	323	2	O650S2	Q650s2 bacteroides
Q89xv0	bradyrhizob	323	2	Q89XV0	Q89xv0 bradyrhizob
Q8up4	pneumocysti	324	2	Q8UUP4	Q8up4 pneumocysti
Q738w6	basillus ce	324	2	Q738W6	Q738w6 basillus ce
Q81r12	basillus an	324	2	Q81R12	Q81r12 basillus an
Q6hjb5	basillus th	325	2	O6HJB5	Q6hjb5 basillus th
Q7vzt6	bordetella	325	2	Q7VZT6	Q7vzt6 bordetella
Q7w574	bordetella	325	2	Q7W574	Q7w574 bordetella
Q7zcq4	bordetella	325	2	Q7ZCQ4	Q7zcq4 bordetella
Q7zz64	brachydanio	325	2	Q7ZZ64	Q7zz64 brachydanio
Q00030	equine herp	326	1	DUT_EHVA	Q00030 equine herp
Q05128	ebola virus	326	1	VP40_EBOZM	Q05128 ebola virus
Q92zr9	rhizobium m	326	2	Q92ZR9	Q92zr9 rhizobium m
Q81dz5	basillus ce	326	2	Q81DZ5	Q81dz5 basillus ce
Q829k7	streptomyc	326	2	Q829K7	Q829k7 streptomyc
Q93251	equid herpe	326	2	O93251	Q93251 equid herpe
Q913a4	zaire ebola	326	2	Q913A4	Q913a4 zaire ebola
Q77dj6	zaire ebola	326	2	Q77DJ6	Q77dj6 zaire ebola
Q9m6r7	pisum sativ	327	2	Q9M6R7	Q9m6r7 pisum sativ

689	6	3.9	327	2	QBULJ3	QBul13 agrobacteri	762	6	3.9	346	2	Q9RWH8	Q9rwh8 deinococcus
690	6	3.9	328	1	ABF2_STRCX	P82594 streptomyc	763	6	3.9	347	2	Q8ZSW1	Q8zsw1 pyrobaculum
691	6	3.9	328	1	NCSR_ARATH	P83291 arabidopsi	764	6	3.9	347	2	Q756V5	Q756v5 ashbya gos
692	6	3.9	328	2	Q9D7H2	Q9d7h2 mus muscu	765	6	3.9	347	2	Q8P334	Q8p334 xanthomonas
693	6	3.9	329	2	O18071	O18071 caenorhabdi	766	6	3.9	347	2	Q8XVZ3	Q8xvz3 ralstonia s
694	6	3.9	329	2	Q9MFE7	Q9mfe7 beta vulgar	767	6	3.9	347	2	Q6A6V2	Q6a6v2 propionibac
695	6	3.9	329	2	Q92T16	Q92t16 rhizobium m	768	6	3.9	347	2	Q72M10	Q72m10 leptospira
696	6	3.9	329	2	Q80PX1	Q80px1 human herpe	769	6	3.9	347	2	Q8A2H5	Q8a2h5 bacteroides
697	6	3.9	329	2	Q80PX2	Q80px2 human herpe	770	6	3.9	349	2	O18110	O18110 caenorhabdi
698	6	3.9	329	2	Q80PX3	Q80px3 human herpe	771	6	3.9	349	2	Q86JV0	Q86jv0 dictyosteli
699	6	3.9	329	2	Q80PX4	Q80px4 human herpe	772	6	3.9	350	2	Q56302	Q56302 thermococcu
700	6	3.9	329	2	Q80PX5	Q80px5 human herpe	773	6	3.9	350	2	Q9XUC5	Q9xuc5 caenorhabdi
701	6	3.9	329	2	Q7T1T5	Q7t1t5 bothrops ja	774	6	3.9	350	2	Q8LEX1	Q8lex1 arabidopsi
702	6	3.9	330	2	Q76852	Q76852 tetranychena	775	6	3.9	350	2	Q93Z83	Q93z83 arabidopsi
703	6	3.9	330	2	Q41402	Q41402 sesbania ro	776	6	3.9	350	2	Q92UN1	Q92un1 arabidopsi
704	6	3.9	331	1	LDHD_LEUMC	P51011 leuconostoc	777	6	3.9	350	2	Q9ZUB9	Q9zub9 arabidopsi
705	6	3.9	331	2	Q6ZFU6	Q6zfu6 oryza sativ	778	6	3.9	350	2	Q7UUP7	Q7uup7 rhodopirell
706	6	3.9	331	2	Q83359	Q83359 treponema p	779	6	3.9	351	2	O81493	O81493 arabidopsi
707	6	3.9	331	2	Q9JIT7	Q9jit7 cavia porce	780	6	3.9	351	2	Q944K0	Q944k0 arabidopsi
708	6	3.9	331	2	Q9JFX9	Q9jfx9 reston ebol	781	6	3.9	352	1	CYAB_STIAU	P40138 stigmatella
709	6	3.9	332	2	Q96ZS5	Q96zs5 sulfolobus	782	6	3.9	352	2	Q6BMG5	Q6bmgs debaryomyce
710	6	3.9	332	2	Q84I39	Q84i39 helicobacte	783	6	3.9	353	2	Q6Z0V7	Q6z0v7 oryza sativ
711	6	3.9	332	2	Q6M925	Q6m925 parachlamyid	784	6	3.9	356	2	Q84I38	Q84i38 helicobacte
712	6	3.9	333	2	O81494	O81494 arabidopsi	785	6	3.9	356	2	Q8NR93	Q8nr93 corynebacte
713	6	3.9	333	2	Q87GV7	Q87gv7 vibrio para	786	6	3.9	356	2	Q7NVD9	Q7nvd9 chromobacte
714	6	3.9	333	2	Q9JST3	Q9jst3 chlamydia p	787	6	3.9	357	2	P78930	P78930 schistosacch
715	6	3.9	333	2	Q9Z6L1	Q9z6l1 chlamydia p	788	6	3.9	357	2	Q74FZ0	Q74fz0 geobacter s
716	6	3.9	334	1	PURR_PASMU	Q9cn88 pasteurella	789	6	3.9	357	2	Q9DF34	Q9df34 brachydanio
717	6	3.9	334	2	O45307	O45307 caenorhabdi	790	6	3.9	358	2	Q8C2A6	Q8c2a6 mus musculu
718	6	3.9	335	2	Q9UZM6	Q9uzm6 pyrococcus	791	6	3.9	358	2	Q6UDM3	Q6udm3 peittacid h
719	6	3.9	335	2	Q7PWN4	Q7pwn4 anopheles g	792	6	3.9	359	1	AROB_CHRVO	Q7nzu4 chromobacte
720	6	3.9	336	1	XRC4_HUMAN	Q13426 homo sapien	793	6	3.9	359	1	HFE_MOUSE	P70387 mus musculu
721	6	3.9	336	2	Q67MQ8	Q67mq8 symbiobacte	794	6	3.9	359	2	Q6N3V1	Q6n3v1 rhodopseudo
722	6	3.9	337	2	O84I37	Q84i37 helicobacte	795	6	3.9	359	2	Q8EYI5	Q8eyi5 leptospira
723	6	3.9	337	2	O58840	O58840 pyrococcus	796	6	3.9	359	2	Q9D754	Q9d754 mus musculu
724	6	3.9	337	2	O8U204	O8u204 pyrococcus	797	6	3.9	361	2	O18068	O18068 caenorhabdi
725	6	3.9	337	2	Q75LX7	Q75lx7 oryza sativ	798	6	3.9	361	2	O8T376	O8t376 meloidogyne
726	6	3.9	337	2	Q84I35	Q84i35 helicobacte	799	6	3.9	362	1	ASG2_YEAST	P1163 saccharomyc
727	6	3.9	337	2	Q73XD2	Q73xd2 mycobacteri	800	6	3.9	362	2	Q6Q5K8	Q6q5k8 saccharomyc
728	6	3.9	337	2	Q89GY5	Q89gy5 bradyrh.zob	801	6	3.9	362	2	Q6Q5K9	Q6q5k9 saccharomyc
729	6	3.9	339	2	Q7MXY9	Q7mxy9 porphyromon	802	6	3.9	362	2	Q7AH88	Q7ah88 escherichia
730	6	3.9	339	2	Q6VZQ0	Q6vzq0 canarypox v	803	6	3.9	362	2	Q6F7E5	Q6f7e5 acinetobact
731	6	3.9	340	2	Q6C875	Q6c875 yarrowia li	804	6	3.9	363	2	Q9NVL6	Q9nvl6 homo sapien
732	6	3.9	340	2	Q69JZ5	Q69jz5 oryza sativ	805	6	3.9	363	2	Q9RKQ5	Q9rkq5 streptomyc
733	6	3.9	340	2	Q8ABQ4	Q8abq4 bacteroides	806	6	3.9	364	2	Q6A6V5	Q6a6v5 propionibac
734	6	3.9	340	2	Q6YCH1	Q6ych1 mus musculu	807	6	3.9	365	1	AROB_PSEPK	Q88cv2 pseudomonas
735	6	3.9	341	2	Q9LMT1	Q9lmt1 arabidopsi	808	6	3.9	365	2	Q8X6B9	Q8x6b9 escherichia
736	6	3.9	341	2	Q6H2J7	Q6h2j7 mycobacteri	809	6	3.9	367	1	AROB_PSESM	Q87v15 pseudomonas
737	6	3.9	341	2	Q6MPL1	Q6mpl1 bdellovibri	810	6	3.9	367	2	O6RCI2	O6rci2 mycobacteri
738	6	3.9	341	2	Q7T5J0	Q7t5j0 cryptophleb	811	6	3.9	367	2	Q7MVZ4	Q7mvz4 porphyromon
739	6	3.9	342	2	Q93KV2	Q93kv2 streptomyc	812	6	3.9	367	2	Q6ZQ44	Q6zq44 mus musculu
740	6	3.9	342	2	Q66IY2	Q66iy2 xenopus lae	813	6	3.9	368	1	AROB_PSEAE	P34002 pseudomonas
741	6	3.9	342	2	Q6DFQ7	Q6dfq7 xenopus tro	814	6	3.9	369	1	HI82_PSEAE	Q9hz68 pseudomonas
742	6	3.9	343	2	O84I34	O84i34 helicobacte	815	6	3.9	369	2	Q979M3	Q979m3 thermoplas
743	6	3.9	343	2	O8Y414	O8y414 listeria mo	816	6	3.9	369	2	Q9HJK0	Q9hjko thermoplas
744	6	3.9	343	2	Q927H6	Q927h6 listeria in	817	6	3.9	369	2	Q84I36	Q84i36 helicobacte
745	6	3.9	343	2	Q71WA8	Q71wa8 listeria mo	818	6	3.9	369	2	O6NIM2	O6nim2 corynebacte
746	6	3.9	344	1	PILT_PSEAE	P24559 pseudomonas	819	6	3.9	370	1	HUPK_RHLIV	P28153 rhizobium l
747	6	3.9	344	2	Q7BTG5	Q7btg5 pseudomonas	820	6	3.9	370	2	O6BRJ2	Q6brj2 debaryomyce
748	6	3.9	344	2	Q9F667	Q9f667 pseudomonas	821	6	3.9	370	2	Q7QQ57	Q7qq57 giardia lam
749	6	3.9	344	2	Q87CD4	Q87cd4 xylella fas	822	6	3.9	370	2	Q9I6T2	Q9i6t2 pseudomonas
750	6	3.9	344	2	Q87V94	Q87v94 pseudomonas	823	6	3.9	371	2	Q93NC0	Q93nc0 mycococcus
751	6	3.9	344	2	Q9PCX1	Q9pcx1 xylella fas	824	6	3.9	371	2	O67JF5	Q67jf5 bacillus su
752	6	3.9	345	1	ADD_RALSO	O8xx15 ralstonia s	825	6	3.9	372	1	DNAJ_BACSU	P17631 bacillus su
753	6	3.9	345	1	CYSA_VIBVU	Q8d653 vibrio vuln	826	6	3.9	372	2	Q8YU49	Q8yua9 anabaena sp
754	6	3.9	345	1	VAOD_YEAST	P32366 saccharomyc	827	6	3.9	373	2	Q8P402	Q8p402 xanthomonas
755	6	3.9	345	2	O8NL23	O8nl23 xanthomonas	828	6	3.9	374	2	Q9PTL7	Q9ptl7 xenopus lae
756	6	3.9	345	2	Q7CLR1	Q7clr1 xanthomonas	829	6	3.9	376	1	Y5D9_GLOVI	Q7ndu3 gloeobacter
757	6	3.9	345	2	Q7PIN4	Q7pin4 chromobacte	830	6	3.9	376	2	Q9Y8P6	Q9y8p6 aeropyrum p
758	6	3.9	346	1	LUXA_PHOFO	P24113 photobacter	831	6	3.9	376	2	Q7PQV5	Q7pqv5 anopheles g
759	6	3.9	346	2	Q97ZH7	Q97zh7 sulfolobus	832	6	3.9	376	2	Q67L31	Q67l31 symbiobactes
760	6	3.9	346	2	Q7WP94	Q7wp94 bordetella	833	6	3.9	376	2	Q6D5Y0	Q6d5y0 erwinia car
761	6	3.9	346	2	Q89LP2	Q89lp2 bradyrhizob	834	6	3.9	376	2	O37387	O37387 common chim

835	376	2	Q801S9	Q801S9 xenopus lae	908
836	377	1	Q8GHY5	Q8ghy5 pseudomonas	909
837	378	1	FLIY_BACSU	P24073 bacillus su	910
838	378	2	Q7X2A0	Q7x2a0 pseudomonas	911
839	380	2	Q6CHZ1	Q6chz1 yarrowia li	912
840	380	2	Q73R97	Q73r97 treponema d	913
841	380	2	Q9K000	Q9k000 neisseria m	914
842	381	1	ARGE_BUCAI	P57155 buchnera ap	915
843	381	2	Q8BIM3	Q8bim3 mus musculus	916
844	384	2	Q6VZP9	Q6vzp9 oryza sativ	917
845	384	2	Q8EX13	Q8ex13 streptomyce	918
846	386	1	ARGJ_CORDI	P62059 corynebacte	919
847	386	1	CUE1_HUMAN	Q9nmw3 homo sapien	920
848	386	2	Q7PK57	Q7pk57 anopheles g	921
849	386	2	Q64094	Q64094 bacterioph	922
850	386	2	Q31927	Q31927 bacillus su	923
851	386	2	Q8BJJ5	Q8bjj5 rhizobium l	924
852	386	2	Q8FEJ4	Q8fej4 acinetobact	925
853	388	1	CUE1_MOUSE	Q8r3v6 mus musculu	926
854	388	2	Q8ZYI9	Q8zyi9 pyrobaculum	927
855	388	2	Q96Z16	Q96z16 sulfolobus	928
856	388	2	Q16881	Q16881 caenorhabdi	929
857	388	2	Q8KE01	Q8ke01 chlorobium	930
858	389	2	Q6LYW7	Q6lyw7 methanococc	931
859	389	2	Q6N4F5	Q6n4f5 rhodopsedo	932
860	389	2	Q89IU8	Q89iu8 bradyrhizob	933
861	389	2	Q8DJV0	Q8djv0 synechococc	934
862	390	2	Q22101	Q22101 caenorhabdi	935
863	391	1	PCL_ECTHA	P42516 ectothiorho	936
864	391	2	Q7JNC6	Q7jnc6 desulfohalob	937
865	391	2	Q7Q6Y4	Q7qgy4 anopheles g	938
866	391	2	Q02690	Q02690 podospora a	939
867	391	2	Q8D5A1	Q8dsa1 vibrio vuln	940
868	392	1	LVC1_YARLI	P41929 yarrowia li	941
869	392	2	Q8Z9Y0	Q8z9y0 oryza sativ	942
870	392	2	Q8GALO	Q8gal0 arthrobacte	943
871	392	2	Q6GLG9	Q6glg9 xenopus tro	944
872	393	2	Q7Y0Z8	Q7y0z8 lycopersico	945
873	393	2	Q8RR83	Q8rr83 acetobacter	946
874	393	2	Q321D8	Q321d8 mus musculu	947
875	394	2	Q8M2N0	Q8m2n0 methylocyst	948
876	394	2	Q8RENE	Q8ren6 fusobacteri	949
877	394	2	Q6A5K4	Q6a5k4 propionibac	950
878	394	2	Q7VVV1	Q7vvv1 bordetella	951
879	394	2	Q7WKJ9	Q7wkj9 bordetella	952
880	394	2	Q8KB99	Q8kb99 bacillus ha	953
881	395	2	Q7XEG1	Q7xeg1 oryza sativ	954
882	395	2	Q6EVS8	Q6evs8 yersinia ps	955
883	395	2	Q9KZC2	Q9kzc2 streptomyce	956
884	396	2	Q6BJ17	Q6bj17 debaryomyce	957
885	397	2	Q3UAU3	Q3uau3 caenorhabdi	958
886	398	2	Q378Z4	Q378z4 thermoplas	959
887	398	2	Q05765	Q05765 saccharomyc	960
888	398	2	Q63R97	Q63r97 burkholderi	961
889	399	2	Q3HGNE	Q3hgn6 schizosacch	962
890	399	2	Q8L912	Q8l912 arabidopsis	963
891	399	2	Q3M9V4	Q3m9v4 arabidopsis	964
892	399	2	Q8BZF1	Q8bzfi mus musculu	965
893	400	2	Q9GZH7	Q9gzh7 caenorhabdi	966
894	400	2	Q6N8Z6	Q6n8z6 rhodopsedo	967
895	400	2	Q73ND4	Q73nd4 treponema d	968
896	400	2	Q6P601	Q6peq1 mus musculu	969
897	401	2	Q8P6E3	Q8pe63 rhizobium l	970
898	401	2	Q7U8J2	Q7u8j2 synechococc	971
899	402	2	Q8KE54	Q8ke54 chlorobium	972
900	402	2	Q7V4M1	Q7v4m1 prochloroco	973
901	402	2	Q6D669	Q6d669 erwinia car	974
902	402	2	Q9W5Z9	Q9w5z9 fugu rubrip	975
903	403	2	Q742P6	Q742p6 mycobacteri	976
904	404	2	Q7QY67	Q7qy67 giardia lam	977
905	404	2	Q7MC72	Q7mc72 vibrio vuln	978
906	405	2	Q97ZT8	Q97zt8 sulfolobus	979
907	405	2	Q9AXJ7	Q9axj7 medicago tr	980

Q8rn03	amycolatops	980
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Q7ps28	anopheles g	912
Q65zt1	borrelia ga	913
Q6jkt4	zootermopsi	914
Q6jkt7	zootermopsi	915
Q9ahf3	lysobacter	916
Q9yct5	aeropyrum p	917
Q9pt10	anopheles g	918
Q7w783	bordetella	919
Q8n6e0	homo sapien	920
Q9hej0	neuropora	921
Q9nal6	caenorhabdi	922
Q6lpk3	photobacter	923
Q7v099	prochloroco	924
Q8lp50	lunaria ann	925
Q6sgb2	uncultured	926
Q7w0p6	bordetella	927
Q7w3f8	bordetella	928
Q7wes8	bordetella	929
Q63h22	bacillus ce	930
Q8liy9	bacillus ce	931
Q81vl5	bacillus an	932
Q8dsq3	streptococc	933
Q9en19	homo sapien	934
Q6rc07	mycobacteri	935
Q64nz1	bacteroides	936
Q91gf4	epiphyas po	937
Q90za4	ambystoma m	938
Q84di2	caulobacter	939
Q84di5	caulobacter	940
Q84di8	caulobacter	941
Q84dj5	caulobacter	942
Q73f05	caulobacter	943
Q8fq6	corynebacte	944
Q6hpj5	bacillus th	945
Q9vz8	methanosarc	946
Q6pvs6	methanosarc	947
Q6x8l3	homo sapien	948
Q86un3	homo sapien	949
Q7we84	bordetella	950
Q83a86	coxiella bu	951
Q6aet0	leifsonia x	952
Q9sx61	arabidopsis	953
Q82017	nitrosomona	954
Q70in2	pseudomonas	955
Q63bu5	bacillus ce	956
Q6f735	acinetobact	957
Q7ul99	rhodopirell	958
Q76652	caenorhabdi	959
Q6jt24	ornithocoon	960
Q8nab8	homo sapien	961
Q76iq2	candida gla	962
Q8as48	encephalito	963
Q7ah4	thermoplas	964
Q7m161	vibrio vuln	965
Q8a5c0	bacteroides	966
Q00770	emericella	967
Q87ly3	vibrio para	968
Q8dbx8	vibrio vuln	969
Q7m2j6	porphyromon	970
Q7cu40	prochloroco	971
Q9ku97	vibrio chol	972
Q94c40	arabidopsis	973
Q9x804	streptomyce	974
P42258	haloarcu	975
Q8ynq2	anabaena sp	976
Q7v019	prochloroco	977
Q9a386	caulobacter	978
Q07364	chlamydia t	979
O84099	chlamydia t	980

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981 6 3.9 434 2 Q823F1 Q823f1 chlamydia m
982 6 3.9 434 2 Q9Pkt9 Q9pkt9 chlamydia m
983 6 3.9 434 2 Q928M2 Q928m2 chlamydia p
984 6 3.9 436 1 R3MB_PSEPK O88r13 pseudomonas
985 6 3.9 436 2 Q86604 O68604 brevibacter
986 6 3.9 438 1 ETIA_XENIA P18755 xenopus lae
987 6 3.9 438 1 TRPE_AERPE Q9Y8t0 aeropyr.am p
988 6 3.9 438 2 Q64CT2 Q64ct2 uncultured
989 6 3.9 438 2 Q50175 Q50175 mycobacteri
990 6 3.9 439 2 Q9V0P1 Q9v0p1 pyrococcus
991 6 3.9 439 2 Q872D8 Q872d8 nemospira
992 6 3.9 439 2 Q6DJL5 Q6dj15 xenopus lae
993 6 3.9 440 1 ETS1_MOUSE P27577 mus musculus
994 6 3.9 440 2 Q50114 Q50114 pyrococcus
995 6 3.9 440 2 Q8VKH9 Q8vkh9 mycobacteri
996 6 3.9 440 2 Q8Y490 Q8y490 listeria mo
997 6 3.9 440 2 Q927S8 Q927s8 listeria in
998 6 3.9 440 2 Q71WL4 Q71wl4 listeria mo
999 6 3.9 440 2 Q8BVW8 Q8bvw8 mus musculus
1000 6 3.9 441 1 ETS1_HUMAN P14921 homo sapien
```

ALIGNMENTS

```
RESULT 1
Q7Z3E6 PRELIMINARY; PRT; 803 AA.
AC Q7Z3E6;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686E1430.
GN Name=DKFZp686E1430;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Human testis;
RC Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL EMBL; BX537955; CAD37922.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR InterPro; IPR003649; Bbox.C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR009061; Putativ_DNA_bind.
DR InterPro; IPR011054; Rudmt_hyb_motif.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00502; BBox; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50144; MATH; 1.
KW Hypothetical protein.
SQ SEQUENCE 803 AA; 89186 MW; 43486E1064478477 CRC64;
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Query Match 100.0%; Score 153; DB 2; Length 803;
Best Local Similarity 100.0%; Pred. No. 3.1e-155;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 FTSELVPSYDSATFVLENFSTLRQADPVYSFQLVSLCWLRLKVPYDPGNGVGRGYLSV 60
|||||
Db 146 FTSELVPSYDSATFVLENFSTLRQADPVYSFQLVSLCWLRLKVPYDPGNGVGRGYLSV 205
|||||
Qy 61 FLELSAGLPETSKYEVYVWVHQSCNDPTKNIREFASDFVGCWGNRFFRLDLLANE 120
|||||
Db 206 FLELSAGLPETSKYEVYVWVHQSCNDPTKNIREFASDFVGCWGNRFFRLDLLANE 265
|||||
Qy 121 GYLNPQNDTVLLRFQVRSPTFFQKSRDQHWYIT 153
|||||
Db 266 GYLNPQNDTVLLRFQVRSPTFFQKSRDQHWYIT 298
|||||
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RESULT 2
Q81YF7 PRELIMINARY; PRT; 964 AA.
AC Q81YF7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE TRIM37 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Testis;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Testis;
RC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC036012; AAH36012.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR003649; Bbox.C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBox; 1.
DR SMART; SM00336; BBox; 1.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 964 AA; 107875 MW; BD63E9177535EB9D CRC64;
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Query Match 100.0%; Score 153; DB 2; Length 964;
Best Local Similarity 100.0%; Pred. No. 3.6e-155;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 FTSELVPSYDSATFVLENFSTLRQADPVYSFQLVSLCWLRLKVPYDPGNGVGRGYLSV 60
|||||
Db 268 FTSELVPSYDSATFVLENFSTLRQADPVYSFQLVSLCWLRLKVPYDPGNGVGRGYLSV 327
|||||
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Qy 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 120
Db 328 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 387

Qy 121 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 153
Db 388 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 420

RESULT 3
Q8WYF7 PRELIMINARY; PRT; 964 AA.
AC Q8WYF7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE POB1.
GN Name=POB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMBL; AB020705; BAA74921.1; -.
DR Genew; HGNC:7523; TRIM37.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50119; ZF_BOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
FT NON TER 1
SQ SEQUENCE 979 AA; 109607 MW; D9958FE2EA23EEFD CRC64;

Query Match 100.0%; Score 153; DB 2; Length 964;
Best Local Similarity 100.0%; Pred. No. 3.6e-155;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSV 60
Db 268 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSV 327

Qy 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 120
Db 328 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 387

Qy 121 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 153
Db 388 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 420

RESULT 4
Q94972 PRELIMINARY; PRT; 979 AA.
AC Q94972;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE KIAA0898 protein (Fragment).
GN Name=KIAA0898;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMBL; AB020705; BAA74921.1; -.
DR Genew; HGNC:7523; TRIM37.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50119; ZF_BOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
FT NON TER 1
SQ SEQUENCE 979 AA; 109607 MW; D9958FE2EA23EEFD CRC64;

Query Match 100.0%; Score 153; DB 2; Length 979;
Best Local Similarity 100.0%; Pred. No. 3.7e-155;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSV 60
Db 283 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSV 342

Qy 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 120
Db 343 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 402

Qy 121 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 153
Db 403 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 435

RESULT 5
Q8CHC5 PRELIMINARY; PRT; 928 AA.
AC Q8CHC5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE KIAA0898 protein (Fragment).
GN Name=KIAA0898;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RA Ohara O., Koga H.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032371; BAC41455.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
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DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR000315; Znf_Bbox.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS00144; MATH; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
FT NON_TER 1
SQ SEQUENCE 928 AA; 103732 MW; 23CEODAAD85BFDE CRC64;

Query Match 81.0%; Score 124; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 5.4e-124;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGVRGYLSV 60
DQ 235 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGVRGYLSV 294
QY 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIIRFASDFEVCWGVNRRFRLDLLANE 120
DQ 295 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIIRFASDFEVCWGVNRRFRLDLLANE 354
QY 121 GYLN 124
DQ 355 GYLN 358

RESULT 6
Q6PCX9 PRELIMINARY; PRT; 961 AA.
AC Q6PCX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tripartite motif protein 37.
GN Name=Trim37;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
```

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RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059070; AAH59070.1; -.
DR EMBL; BC058678; AAH58678.1; -.
DR GO; GO:0016015; F:morphogen activity; TAS.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS00144; MATH; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 961 AA; 107659 MW; 85629CFE0A1D6EA CRC64;

Query Match 81.0%; Score 124; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 5.5e-124;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGVRGYLSV 60
DQ 268 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGVRGYLSV 327
QY 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIIRFASDFEVCWGVNRRFRLDLLANE 120
DQ 328 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIIRFASDFEVCWGVNRRFRLDLLANE 387
QY 121 GYLN 124
DQ 388 GYLN 391

RESULT 7
Q95LM3 PRELIMINARY; PRT; 721 AA.
AC Q95LM3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RA "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
in the human genome sequence."
BMC Genomics 3:36-36(2002).
DR EMBL; AB071078; BAB64471.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; P:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR001841; Znf_Ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 721 AA; 80131 MW; 203B974760F866E9 CRC64;
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Query Match 51.6%; Score 79; DB 2; Length 721;
 Best Local Similarity 100.0%; Pred. No. 1e-75;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 EYRVMHQSCNDPTKNIIRFASDFEVEGCGWYNNRFRLLDANEGYLNPNQDVTILRF 134
 Db 100 EYRVMHQSCNDPTKNIIRFASDFEVEGCGWYNNRFRLLDANEGYLNPNQDVTILRF 159

Qy 135 QVRSPTFPQKSRDQHWYIT 153
 Db 160 QVRSPTFPQKSRDQHWYIT 178

RESULT 8
 ID G101 HUMAN STANDARD; PRT; 508 AA.
 AC Q96P66; QNGG93;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Probable G protein-coupled receptor GPR101.
 GN Name=GPR101;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
 RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
 RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
 RT "Discovery and mapping of ten novel G protein-coupled receptor
 genes";
 RL Gene 275:83-91(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
 RA Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;
 RT "Identification of G protein-coupled receptor genes from the human
 genome sequence";
 RL FEBS Lett. 520:97-101(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Teutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.ebi.ac.uk/ebis-sib.ch>)
 or send an email to license@ebi-sib.ch.

EMBL; AF411115; AAL26486.1; --
 EMBL; AB083588; BAB89301.1; --
 EMBL; AB065937; BAC06152.1; ALT_INIT.
 Genew; HGNC:14963; GPR101.
 MIM; 300393; --
 InterPro; IPR000276; GPCR_Rhodpsn.
 Pfam; PF00001; 7tm 1; 1.
 PRINTS; PF00237; GPCR_Rhodopsin.
 PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 DOMAIN 1 35 Extracellular (Potential).

TRANSMEM 36 56 1 (Potential).
 DOMAIN 57 68 Cytoplasmic (Potential).
 FT 69 89 2 (Potential).
 FT 90 106 Extracellular (Potential).
 FT 107 127 3 (Potential).
 FT 128 149 Cytoplasmic (Potential).
 FT 150 170 4 (Potential).
 FT 171 196 Extracellular (Potential).
 FT 197 217 5 (Potential).
 FT 218 399 Cytoplasmic (Potential).
 FT 400 420 6 (Potential).
 FT 421 433 Extracellular (Potential).
 FT 434 454 7 (Potential).
 FT 455 508 Cytoplasmic (Potential).
 FT DISULFID 104 182 By similarity.
 FT CARBOHYD 7 7 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 508 AA; 56716 MW; E20A409F5C95BBS CRC64;

Query Match 5.9%; Score 9; DB 1; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VPSYDSATP 14
 Db 499 VPSYDSATP 507

RESULT 9
 O34947 PRELIMINARY; PRT; 210 AA.
 ID O34947
 AC O34947; O796E9;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Yoaz.
 GN Name=Yoaz; OrderedLocusNames=BSU18790;
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
 RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Gim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Haelegh J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
 RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klacker-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
 RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
 RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maue C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
 RA Park S.H., Parro T., Pohl T.M., Portetelle D., Porwollik S.,
 RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
 RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
 RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serfor P.,
 RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenberg M., Vannier F.,

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RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
DR EMBL; AF027868; AAB84456.1; -.
DR EMBL; Z99114; CAB13771.1; -.
DR PIR; A69898; A69898.
DR InterPro; IPR002818; ThiJ/Pfpi.
DR Pfam; PF01965; DJ_1_pfp1; 1.
KW Complete proteome.
SQ SEQUENCE 210 AA; 23420 MW; 18A8BA915AAEF745 CRC64;

Query Match 5.2%; Score 8; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LANEGYLN 124
Db 116 LANEGYLN 123

RESULT 10
Q65003 PRELIMINARY; PRT; 286 AA.
ID Q65003;
AC Q65003;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative cell-to-cell movement protein.
OS Apple mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=12319;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95374352; PubMed=7646355;
RA Shiel P.J., Alrfai R.H., Domier L.L., Korban S.S., Berger P.H.;
RT "The complete nucleotide sequence of apple mosaic virus RNA-3.";
RL Arch. Virol. 140:1247-1256(1995).
DR EMBL; U15608; AAB86960.1; -.
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP; 1.
SQ SEQUENCE 286 AA; 32409 MW; D2A4493315AB82C1 CRC64;

Query Match 5.2%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 SDFEVGEC 105
Db 10 SDFEVGEC 17

RESULT 11
Q63CU1 PRELIMINARY; PRT; 423 AA.
ID Q63CU1;
AC Q63CU1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chlorohydrolase/deaminase family protein.
GN ORFNames=BTZK1601;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ZK;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,

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RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18572.1; -.
KW Hydrolase.
SQ SEQUENCE 423 AA; 46816 MW; BD583BC7F209A87B CRC64;

Query Match 5.2%; Score 8; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 EFASDREV 102
Db 27 EFASDREV 34

RESULT 12
Q81S14 PRELIMINARY; PRT; 435 AA.
ID Q81S14; Q61094; Q6K068;
AC Q81S14; Q61094; Q6K068;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chlorohydrolase family protein.
GN OrderedLocustNames=BA1865; BA1729; GBAA1865;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapfel E.K., Ostad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Platt R.D., Wolf A.M., Watkins K.L., Niernan W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017030; AAP25768.1; -.
DR EMBL; AE017334; AAT30980.2; -.
DR EMBL; AE017225; AAT54045.1; -.
DR HSP; O9X034; 1p1M.
DR TIGR; BA1865; -.
DR TIGR; GBAA1865; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro 1.
DR InterPro; IPR011550; Amidohydro like.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro 1; 1.
DR ProDom; PD001248; Amidohydro_like; 1.

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KW Complete proteome; Hydrolase.
SQ SEQUENCE 435 AA; 48143 MW; 2D9289BAA5819B33 CRC64;
Query Match 5.2%; Score 8; DB 2; Length 435;
Best Local Similarity 100.0%; Pred.No.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 95 EFASDFEV 102
Db 39 EFASDFEV 46
RESULT 13
Q6HK87 PRELIMINARY; PRT; 435 AA.
AC Q6HK87;
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Chlorohydrolase/deaminase family protein.
GN OrderedLocustNames=BT9727.1707;
OS Bacillus thuringiensis (Subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.P., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Kelm P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE017355; AAT59611.1; -;
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR006680; Amidohydro_1.
DR InterPro: IPR011550; Amidohydro_like.
DR Pfam: PF01979; Metallo hydrolase.
DR ProDom: PD01248; Amidohydro_1; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 435 AA; 48139 MW; 6BEE505358AE3268 CRC64;
Query Match 5.2%; Score 8; DB 2; Length 435;
Best Local Similarity 100.0%; Pred.No.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 95 EFASDFEV 102
Db 39 EFASDFEV 46
RESULT 14
Q8E8R3 PRELIMINARY; PRT; 1045 AA.
AC Q8E8R3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heavy metal efflux pump, CzcA family.
GN OrderedLocustNames=SO4598;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbr749;
RA Heidelberg J.P., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R., Meyer T., Teapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Unayam L.A.,

RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL: AE015891; AAN57558.1; -;
DR TIGR: SO4598; -;
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0008324; F:cation transporter activity; IEA.
DR GO: GO:0006812; P:cation transport; IEA.
DR InterPro: IPR003439; ABC transporter.
DR InterPro: IPR001036; Acrflavin_res.
DR InterPro: IPR004763; CzcA.
DR Pfam: PF00873; Acr tran; 1.
DR PRINTS: PRO0702; ACRIFLAVINRP.
DR TIGRFAMs: TIGR00914; ZAO601; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1045 AA; 114513 MW; 9E99187C3248C984 CRC64;
Query Match 5.2%; Score 8; DB 2; Length 1045;
Best Local Similarity 100.0%; Pred.No.32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 63 ELSAGLPE 70
Db 311 ELSAGLPE 318
RESULT 15
Q89T67 PRELIMINARY; PRT; 98 AA.
AC Q89T67;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bel2183 protein.
GN OrderedLocustNames=bsl2183;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL: AP005942; BAC47448.1; -;
KW Complete proteome.
SQ SEQUENCE 98 AA; 10886 MW; 90279D1E01E99AD5 CRC64;
Query Match 4.6%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred.No.45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 127 NDTVILR 133
Db 39 NDTVILR 45
Search completed: July 20, 2005, 20:51:41
Job time : 143.45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:37:15 ; Search time 87.75 Seconds
(without alignments)
787.814 Million cell updates/sec

Title: US-09-706-325-25
Perfect score: 135
Sequence: 1 ELVPSYDSATVLENFSTLR.....NEGYLNPNQDVTILRFQVRS 135

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135	100.0	803	2	Q7Z3E6
2	135	100.0	964	2	Q81YF7
3	135	100.0	964	2	Q8WYF7
4	135	100.0	979	2	Q84972
5	121	89.6	928	2	Q8CHCS
6	121	89.6	961	2	Q6PCX9
7	64	47.4	721	2	Q95LW3
8	9	6.7	508	1	G101_HUMAN
9	8	5.9	210	2	Q34947
10	8	5.9	286	2	Q85003
11	8	5.9	423	2	Q63CU1
12	8	5.9	435	2	Q81S14
13	8	5.9	435	2	Q6HK87
14	8	5.9	1045	2	Q8E8R3
15	7	5.2	98	2	Q89T67
16	7	5.2	124	2	Q82117
17	7	5.2	174	2	Q7P7W8
18	7	5.2	198	2	Q46025
19	7	5.2	198	2	Q6NGT3
20	7	5.2	233	2	Q7UJZ9
21	7	5.2	246	2	Q82FC0
22	7	5.2	253	2	Q9XAL5
23	7	5.2	255	2	Q74D44
24	7	5.2	257	2	Q9WXV4
25	7	5.2	261	2	Q70EC9
26	7	5.2	278	2	Q7UEF2
27	7	5.2	285	2	Q90ZA2
28	7	5.2	307	2	Q87TD8
29	7	5.2	316	2	Q9XWH8
30	7	5.2	318	2	Q7T2H3
31	7	5.2	319	2	Q8KJCI

Q98k82 rhizobium 1
Q81n26 bacillus an
Q6hg72 bacillus th
Q813b9 bacillus ce
Q8brb6 mus musculu
Q92n54 rhizobium m
Q889p7 pseudomonas
Q8r831 thermotoga
Q8nuc9 corynebacte
Q6a7r5 propionibac
Q8g211 brucella su
Q8yfw9 brucella me
Q6ipl4 homo sapien
Q7qbx7 anopheles g
Q9v792 drosophila
Q6cgz2 streptomyce
Q6cgz2 yarrowia li
Q6vub6 marincococ
Q8erp3 oceanobacil
Q6rjg6 halobacillu
Q6iuv3 halobacillu
Q631b3 bacillus ce
Q72xl8 bacillus ce
Q81sc6 bacillus ce
Q81k57 bacillus an
Q8et62 oceanobacil
Q6hb48 bacillus th
Q929s7 listeria in
Q71x82 listeria mo
Q9x4a5 listeria mo
Q7rx54 neurospora
Q62rf3 bacillus li
Q7nq38 chromobacte
P54417 bacillus su
Q65fz6 bacillus li
Q6vth4 marincococ
Q8cp3 staphylococ
Q7x226 staphylococ
Q931s4 staphylococ
Q99uc9 staphylococ
Q7a0z0 staphylococ
Q6g9l0 staphylococ
Q6gh56 staphylococ
Q7pwv8 anopheles g
Q8bh92 m mus muscu
Q8c3c6 mus musculu
Q8c3w8 mus musculu
Q6ppg3 chlamydomon
Q6zpw4 mus musculu
Q62pw4 mus musculu
Q64mu8 bacteroides
Q813x9 bacillus ce
Q753y3 ashbya goas
Q755j3 ashbya goas
Q9h4f0 homo sapien
Q9nyv6 homo sapien
Q7mv63 porphyromon
Q7r282 giardia lam
Q9x1l9 arabidopsis
Q6zou0 oryza sativ
Q8541 hordeum vul
Q9fyo hordeum vul
Q81k09 plasmodium
Q9s7s8 hordeum vul
Q8sja2 escherichia
Q7wud4 escherichia
Q7oct4 arabidopsis
Q7uub8 rhodopirell
Q81341 plasmodium

105	7	5.2	1351	2	Q8XZ58	Q8xz58	ralstonia s
106	7	5.2	1369	2	Q6NZJ7	Q6nzj7	mus musculus
107	7	5.2	1390	2	Q8r6H6	Q8t6h6	dictyosteli
108	7	5.2	1777	2	Q89278	Q89278	himetobi p
109	7	5.2	1777	2	Q6F3H3	Q6f3h3	xanthomoni p
110	7	5.2	2224	2	Q8P8Y4	Q8p8y4	hathomonas
111	7	5.2	3805	2	Q7Y1L1	Q7y1l1	cryptospori
112	7	5.2	4578	2	Q42181	Q42181	fugu rubrip
113	7	5.2	13536	2	Q83VS0	Q83vs0	pseudomonas
114	6	4.4	31	2	Q76030	Q76030	homo sapien
115	6	4.4	38	2	Q7R6R2	Q7r6r2	giardia lam
116	6	4.4	38	2	Q04102	Q04102	rattus norv
117	6	4.4	40	2	Q33162	Q33162	methanosarc
118	6	4.4	44	2	Q06684	Q06684	treponema d
119	6	4.4	47	2	Q73198	Q73198	wolbachia p
120	6	4.4	50	2	Q6VEQ9	Q6veq9	mycobacteri
121	6	4.4	54	2	Q75QM5	Q75qm5	bacteriophi
122	6	4.4	54	2	Q9F6K7	Q9f6k7	borrelia ga
123	6	4.4	56	2	Q70BFB	Q70bfb	bacteriophi
124	6	4.4	58	2	Q6KAW2	Q6kaw2	pneumocysti
125	6	4.4	61	2	Q7Z763	Q7z763	homo sapien
126	6	4.4	61	2	Q9F6K8	Q9f6k8	borrelia ga
127	6	4.4	62	2	Q7Y3G0	Q7y3g0	streptococc
128	6	4.4	62	2	Q9ETG1	Q9etg1	borrelia ga
129	6	4.4	64	2	Q7R130	Q7r130	plasmodium
130	6	4.4	64	2	Q41403	Q41403	sebsania ro
131	6	4.4	65	2	Q9F6C5	Q9f6c5	borrelia ga
132	6	4.4	66	2	Q6RUP9	Q6rup9	homo sapien
133	6	4.4	71	2	Q96W62	Q96w62	pneumocysti
134	6	4.4	71	2	Q96W63	Q96w63	pneumocysti
135	6	4.4	71	2	Q96W64	Q96w64	pneumocysti
136	6	4.4	71	2	Q96W65	Q96w65	pneumocysti
137	6	4.4	71	2	Q96W66	Q96w66	pneumocysti
138	6	4.4	71	2	Q96W67	Q96w67	pneumocysti
139	6	4.4	77	2	Q97W40	Q97w40	sulfolobus
140	6	4.4	79	2	Q9P935	Q9p935	clonostachy
141	6	4.4	80	2	Q6Z1J5	Q6zijs	oryza sativ
142	6	4.4	81	2	Q9XGY1	Q9xgy1	lycopersico
143	6	4.4	83	2	Q7MJA7	Q7mja7	vibrio vuln
144	6	4.4	83	2	Q7MNB2	Q7mnb2	vibrio vuln
145	6	4.4	84	2	Q67IS6	Q67is6	oryza sativ
146	6	4.4	85	2	Q7RM06	Q7rm06	plasmodium
147	6	4.4	85	2	Q9XHG3	Q9xhg3	arabidopsis
148	6	4.4	86	2	Q49969	Q49969	solanum tub
149	6	4.4	86	2	Q6VER6	Q6ver6	mycobacteri
150	6	4.4	86	2	Q9F6K6	Q9f6k6	borrelia ga
151	6	4.4	87	2	Q6PBH7	Q6pbh7	brachydanio
152	6	4.4	89	2	Q911T3	Q911t3	pseudomonas
153	6	4.4	90	2	Q709B9	Q709b9	human immun
154	6	4.4	94	2	Q8RJN0	Q8rjn0	streptomyce
155	6	4.4	97	2	Q87GH3	Q87gh3	vibrio para
156	6	4.4	97	2	Q8E3A3	Q8e3a3	streptococc
157	6	4.4	98	2	Q24186	Q24186	oryza sativ
158	6	4.4	98	2	Q8H3I7	Q8h3i7	oryza sativ
159	6	4.4	98	2	Q6AQ57	Q6aq57	desulfotale
160	6	4.4	101	2	Q49968	Q49968	solanum tub
161	6	4.4	101	2	Q81UH7	Q81uh7	bacillus an
162	6	4.4	102	1	R310_TREDE	Q83218	treponema d
163	6	4.4	102	1	R510_TREPA	Q83218	treponema p
164	6	4.4	102	2	Q14278	Q14278	homo sapien
165	6	4.4	102	2	Q811X0	Q81lx0	plasmodium
166	6	4.4	105	2	Q6MY55	Q6mys5	aspergillus
167	6	4.4	105	2	Q6AP72	Q6ap72	desulfotale
168	6	4.4	106	2	Q89S46	Q89s46	bradyrhizob
169	6	4.4	108	2	Q63FB0	Q63fb0	bacillus ce
170	6	4.4	108	2	Q73CT3	Q73ct3	bacillus ce
171	6	4.4	108	2	Q6HMT4	Q6hmt4	bacillus th
172	6	4.4	109	2	Q6YXJ4	Q6yxj4	oryza sativ
173	6	4.4	109	2	Q81HB7	Q81hb7	bacillus ce
174	6	4.4	110	2	Q9ARX7	Q9arx7	oryza sativ
175	6	4.4	111	2	Q976I2	Q976i2	sulfolobus
176	6	4.4	113	2	Q6NC40	Q6nc40	rhodopsendo
177	6	4.4	114	2	Q7QLA1	Q7qla1	anopheles g

P90861	2	116	2	P90861	caenorhabdi
Q989A4	2	116	2	Q989A4	vicia faba
P76196	1	118	1	YDIL_ECOLI	escherichia
Q654K8	2	118	2	Q654K8	oryza sativ
Q70AH2	2	118	2	Q70AH2	shigella fl
Q80117	2	118	2	Q80117	petromyzon
Q6N539	2	119	2	Q6N539	rhodopsendo
Q8bxt4	2	119	2	Q8bxt4	mus musculus
Q7qzb7	2	120	2	Q7qzb7	giardia lam
Q94es4	2	120	2	Q94ES4	pisum sativ
Q729Y5	2	120	2	Q729Y5	desulfovibr
Q9w218	2	121	2	Q9W218	prosophila
Q6AAH7	2	121	2	Q6AAH7	propionibac
Q6d2q0	2	123	2	Q6D2Q0	erwinia car
Q86u47	2	124	2	Q86U47	homo sapien
Q66030	2	124	2	Q66030	chlamydia s
Q06566	2	124	2	Q06566	mycobacteri
Q7u0M4	2	124	2	Q7U0M4	mycobacteri
Q6mdm6	2	124	2	Q6MDM6	parachlamyd
Q8tm09	2	126	2	Q8TM09	methanosarc
Q83kv9	2	126	2	Q83KV9	shigella fl
Q8fh45	2	127	2	Q8FH45	escherichia
Q8x5Y6	2	127	2	Q8X5Y6	escherichia
Q929D4	2	129	2	Q929D4	listeria in
Q82NH2	2	129	2	Q82NH2	streptomyce
Q8bjx7	2	129	2	Q8BJX7	mus musculu
Q29186	2	130	2	Q29186	archaeoglob
Q7mm63	2	130	2	Q7MM63	vibrio vuln
Q87na2	2	130	2	Q87NA2	vibrio para
Q8d8a5	2	130	2	Q8D8A5	vibrio vuln
Q9acy7	2	130	2	Q9ACY7	streptomyce
Q8q0t6	2	131	2	Q8Q0T6	methanosarc
Q8y535	2	131	2	Q8Y535	listeria mo
Q71xc4	2	131	2	Q71XC4	listeria mo
Q82L93	2	132	2	Q82L93	streptomyce
Q89bg1	2	132	2	Q89BQ1	bradyrhizob
Q9lt36	2	132	2	Q9LT36	arabidopsis
Q7p1m0	2	135	2	Q7P1M0	anopheles g
Q9fc41	2	135	2	Q9FC41	streptomyce
Q54938	2	136	2	Q54938	ondatra zib
Q94es3	2	137	2	Q94ES3	pisum sativ
Q729e0	2	138	2	Q729E0	desulfovibr
Q61zb3	2	141	2	Q6LZB3	methanococc
Q9y244	2	141	2	Q9Y244	homo sapien
Q7qzp8	2	141	2	Q7QZP8	giardia lam
Q9cxb8	2	141	2	Q9CXV8	mus musculu
Q9czl7	2	141	2	Q9CZL7	mus musculu
Q9cqt5	2	141	2	Q9CQT5	m mus muscu
Q8ptq2	2	142	2	Q8PTQ2	methanosarc
Q67uq6	2	142	2	Q67UQ6	oryza sativ
Q8kg57	2	142	2	Q8KG57	chlorobium
Q6zqs0	2	143	2	Q6ZQS0	homo sapien
Q08439	2	144	2	Q08439	saccharomyc
Q8abf9	2	144	2	Q8ABF9	bacteroides
Q8knp6	2	145	2	Q8KNP6	bacillus th
Q88v63	2	146	2	Q88V63	uncultured
Q68v64	2	146	2	Q68V64	uncultured
Q68v67	2	146	2	Q68V67	uncultured
Q68v68	2	146	2	Q68V68	uncultured
Q68v72	2	146	2	Q68V72	uncultured
Q68v73	2	146	2	Q68V73	uncultured
Q68v74	2	146	2	Q68V74	uncultured
Q68v79	2	146	2	Q68V79	uncultured
Q68v80	2	146	2	Q68V80	uncultured
Q93nf3	2	147	2	Q93NF3	arthrobacte
Q32m26	2	147	2	Q32M26	rhizobium m
Q737p5	2	147	2	Q737P5	bacillus ce
Q22500	2	148	2	Q22500	caenorhabdi
Q6ah32	1	149	1	Y281_LEIXX	leifsonia x
Q89012	2	149	2	Q89012	lactobacill
Q66086	2	150	2	Q66086	canine hearp
Q64a10	2	153	2	Q64A10	uncultured

251	6	4.4	153	2	Q8YJQ9	Q8YJQ9 brucella me	324	6	4.4	191	1	PTH_MYCBO	P65866 mycobacteri
252	6	4.4	154	2	Q7M1Z7	Q7m1z7 daucus caro	325	6	4.4	191	1	PTH_MYCTU	P65865 mycobacteri
253	6	4.4	154	2	Q7XZ67	Q7xz67 griffithsia	326	6	4.4	191	2	Q741V9	Q741v9 mycobacter
254	6	4.4	155	2	Q7VP20	Q7vp20 haemophilus	327	6	4.4	193	1	YN42_CAUCR	Q9a5v5 caulobacter
255	6	4.4	157	2	Q8DXN3	Q8dxn3 streptococc	328	6	4.4	193	2	Q9NX89	Q9nx89 homo sapien
256	6	4.4	158	2	Q8XQL8	Q8xql8 raistonia s	329	6	4.4	194	2	Q66080	Q66080 canine harp
257	6	4.4	158	2	Q7VL01	Q7vl01 haemophilus	330	6	4.4	196	2	Q6FDU6	Q6fdud acinetobact
258	6	4.4	159	2	P73640	P73640 synechocyst	331	6	4.4	196	2	Q83DI8	Q83dl8 coxiella bu
259	6	4.4	160	2	Q7N1H1	Q7nh1 photorhabdu	332	6	4.4	197	2	Q7VZ32	Q7vz32 drosophila
260	6	4.4	161	1	RL11_METWA	Q8py53 methanosarc	333	6	4.4	198	2	Q7RV81	Q7rvr1 neurospora
261	6	4.4	161	2	Q8U4L4	Q8u4l4 pyrococcus	334	6	4.4	198	2	Q6VY95	Q6vy95 oryza sativ
262	6	4.4	161	2	Q9HB69	Q9hb69 homo sapien	335	6	4.4	199	1	PTH_MYCLE	Q8cd49 mycobacteri
263	6	4.4	161	2	Q32085	Q32085 bacillus su	336	6	4.4	199	2	Q8PA66	Q8pa66 xanthomonas
264	6	4.4	161	2	Q7ME07	Q7me07 vibrio vuln	337	6	4.4	200	2	Q9PX32	Q9px32 human herpe
265	6	4.4	161	2	Q7WE75	Q7we75 bordetella	338	6	4.4	200	2	Q9W8K2	Q9w8k2 human herpe
266	6	4.4	161	2	Q6S9W2	Q6s9w2 columbid ci	339	6	4.4	200	2	Q9YUA9	Q9yu9 human immun
267	6	4.4	162	2	Q64EG2	Q64eg2 uncultured	340	6	4.4	201	2	Q7QNV9	Q7qnv9 giardia lam
268	6	4.4	162	2	Q87Z67	Q87z67 pseudomonas	341	6	4.4	201	2	Q7YXH2	Q7yxh2 caenorhabdi
269	6	4.4	164	2	Q05127	Q05127 neisseria g	342	6	4.4	202	2	Q6V0K5	Q6v0k5 mycobacteri
270	6	4.4	165	2	Q98LE9	Q98le9 rhizobium l	343	6	4.4	203	2	Q9KMZ7	Q9kmz7 vibrio chol
271	6	4.4	165	2	Q747H7	Q747h7 geobacter s	344	6	4.4	204	2	Q9RC46	Q9rc46 bacillus ha
272	6	4.4	166	2	Q6XND3	Q6xnd3 rhodococcus	345	6	4.4	204	2	Q98HN0	Q98hn0 rhizobium l
273	6	4.4	171	1	YCBV_ECOLI	P75860 escherichia	346	6	4.4	205	2	Q8ID59	Q8id59 plasmodium
274	6	4.4	171	2	Q8PHF9	Q8phf9 xanthomonas	347	6	4.4	205	2	Q9HZD9	Q9hzd9 pseudomonas
275	6	4.4	171	2	Q82N41	Q82n41 streptomyce	348	6	4.4	206	1	YX59_PSESM	Q87zr5 pseudomonas
276	6	4.4	172	2	Q87CK2	Q87ck2 xylella fas	349	6	4.4	206	2	Q74N80	Q74n80 nanoarchaeu
277	6	4.4	172	2	Q9I2Q0	Q9i2q0 pseudomonas	350	6	4.4	206	2	Q7PIX6	Q7pix6 anopheles g
278	6	4.4	175	2	Q84R71	Q84r71 oryza sativ	351	6	4.4	206	2	Q86EJ3	Q86ej3 schistosoma
279	6	4.4	177	2	Q81RP2	Q81rp2 drosophila	352	6	4.4	206	2	Q8BRQ1	Q8brq1 mus musculus
280	6	4.4	178	2	Q82Y10	Q82y10 pyrobaculum	353	6	4.4	208	1	Y4B5_PSEPK	Q88fr8 pseudomonas
281	6	4.4	178	2	Q87051	Q87051 pseudocardi	354	6	4.4	208	2	Q8H014	Q8h014 oryza sativ
282	6	4.4	178	2	Q87568	Q87568 helicobacte	355	6	4.4	208	2	Q8YHJ5	Q8yhj5 bruceella me
283	6	4.4	178	2	Q8CR93	Q8cr93 staphylococ	356	6	4.4	209	1	GEMI_HUMAN	Q75496 homo sapien
284	6	4.4	178	2	Q8A5S1	Q8a5s1 caulobacter	357	6	4.4	211	2	Q8BSI3	Q8bsi3 mus musculus
285	6	4.4	179	2	Q7QIN0	Q7qin0 anopheles g	358	6	4.4	212	2	Q9C9K9	Q9c9k9 arabidopsis
286	6	4.4	179	2	Q87VN0	Q87vn0 pseudomonas	359	6	4.4	212	2	Q85372	Q85372 rhodococcus
287	6	4.4	179	2	Q88HE4	Q88he4 pseudomonas	360	6	4.4	213	2	Q65EF8	Q65ef8 bacillus li
288	6	4.4	179	2	Q9QUC6	Q9quc6 tt virus. o	361	6	4.4	213	2	Q7UWS1	Q7uws1 rhodopirell
289	6	4.4	180	2	Q50971	Q50971 neisseria g	362	6	4.4	214	2	Q7Q2M4	Q7q2m4 anopheles g
290	6	4.4	180	2	Q8G0B3	Q8g0b3 brucella su	363	6	4.4	214	2	Q657Y6	Q657y6 oryza sativ
291	6	4.4	181	2	Q74KA6	Q74ka6 lactobacill	364	6	4.4	215	1	RPB5_CANGA	Q65qa6 candida gla
292	6	4.4	181	2	Q7DD77	Q7dd77 neisseria m	365	6	4.4	215	1	RPB5_YEAST	P20434 saccharomyc
293	6	4.4	181	2	Q9JQN6	Q9jqn6 neisseria m	366	6	4.4	215	2	Q9XEX0	Q9xex0 gracilaria
294	6	4.4	182	2	Q04410	Q04410 raphanus sa	367	6	4.4	215	2	Q8X4E4	Q8x4e4 escherichia
295	6	4.4	182	2	Q6RVZ1	Q6rvz1 bifidobacte	368	6	4.4	217	2	Q72A59	Q72a59 desulfovibr
296	6	4.4	182	2	Q8DJX9	Q8djx9 synechococc	369	6	4.4	218	1	YD12_MYCPN	P75469 mycoplasma
297	6	4.4	183	1	DIN1_RAPSA	P27626 raphanus sa	370	6	4.4	218	2	Q754S6	Q754s6 ashbya gosb
298	6	4.4	183	2	Q21131	Q21131 caenorhabdi	371	6	4.4	219	2	Q9AS64	Q9as64 oryza sativ
299	6	4.4	183	2	Q9HXU2	Q9hxu2 pseudomonas	372	6	4.4	222	2	Q7WGT6	Q7wgt6 bordetella
300	6	4.4	184	2	Q8JF87	Q8jf87 human immun	373	6	4.4	223	2	Q972K5	Q972k5 sulfolobus
301	6	4.4	185	2	Q8A357	Q8a357 bacteroides	374	6	4.4	223	2	Q7VT24	Q7vtz4 bordetella
302	6	4.4	186	1	RRF_RHOBA	Q7uch0 rhodopirell	375	6	4.4	223	2	Q7WK92	Q7wk92 bordetella
303	6	4.4	186	1	TNR5_PSEAE	P06691 pseudomonas	376	6	4.4	224	2	Q82M30	Q82m30 streptomyce
304	6	4.4	186	1	TNR7_ECOLI	P06692 escherichia	377	6	4.4	224	2	Q9RU88	Q9ru88 deinococcus
305	6	4.4	186	2	Q66046	Q66046 pseudomonas	378	6	4.4	225	2	Q9ZBV3	Q9zbv3 streptomyce
306	6	4.4	186	2	Q934S3	Q934s3 thiobacillu	379	6	4.4	226	2	Q33188	Q33188 mycobacteri
307	6	4.4	186	2	Q8BE60	Q8be60 aeromonas p	380	6	4.4	226	2	Q7TZS6	Q7tzes6 mycobacteri
308	6	4.4	186	2	Q7AXT9	Q7axt9 pseudomonas	381	6	4.4	227	2	Q6C587	Q6c587 yarrowia li
309	6	4.4	186	2	Q7BEI7	Q7bei7 shigella fl	382	6	4.4	227	2	Q7MUR2	Q7mur2 porphyromon
310	6	4.4	186	2	Q9AJD0	Q9ajd0 pseudomonas	383	6	4.4	227	2	Q9RWX2	Q9rwx2 deinococcus
311	6	4.4	186	2	Q65IT1	Q65it1 bacillus li	384	6	4.4	230	1	AQPZ_PSEPK	Q88f17 pseudomonas
312	6	4.4	187	2	Q7AG38	Q7ag38 escherichia	385	6	4.4	230	1	UL16_HCMVA	P16757 human cytom
313	6	4.4	187	2	Q8X581	Q8x581 escherichia	386	6	4.4	230	2	Q7MF87	Q7mf87 human cytom
314	6	4.4	187	2	Q83RX8	Q83rx8 shigella fl	387	6	4.4	230	2	Q7TF85	Q7tf85 human cytom
315	6	4.4	188	2	Q30134	Q30134 archaeoglob	388	6	4.4	231	2	Q67SV4	Q67sv4 symbiobacte
316	6	4.4	188	2	P73277	P73277 synechocyst	389	6	4.4	232	2	Q9LAS2	Q9las2 desulfitoba
317	6	4.4	188	2	Q9JL38	Q9jl38 mus musculu	390	6	4.4	232	2	Q8ZN09	Q8zn09 salmoneella
318	6	4.4	189	2	Q74323	Q74323 s signal pe	391	6	4.4	232	2	Q741I1	Q741i1 lactobacill
319	6	4.4	189	2	Q8A356	Q8a356 bacteroides	392	6	4.4	233	2	P78728	P78728 pneumocysti
320	6	4.4	189	2	Q9FCH8	Q9pch8 xylella fas	393	6	4.4	233	2	P78730	P78730 pneumocysti
321	6	4.4	190	1	CYGB_HUMAN	Q8wmm9 homo sapien	394	6	4.4	233	2	Q6TLZ5	Q6tlz5 mycobacteri
322	6	4.4	190	2	Q8N2X5	Q8n2x5 homo sapien	395	6	4.4	233	2	Q92Z40	Q92z40 rhizobium m
323	6	4.4	190	2	Q8GHN3	Q8ghn3 pseudomonas	396	6	4.4	233	2	Q7NGN2	Q7ngn2 gloeobacter

397	6	4.4	233	2	Q9TV64	Q9jv64 neisseria m	470	6	4.4	261	2	Q6L711	Q6l71l buergeria b
398	6	4.4	233	2	Q9K054	Q9k054 neisseria m	471	6	4.4	261	2	Q7VSU8	Q7vsj8 bordetella
399	6	4.4	234	1	SNG1_MOUSE	O43759 homo sapien	472	6	4.4	261	2	Q7W459	Q7w459 bordetella
400	6	4.4	234	1	SNG1_MOUSE	O55100 mus musculus	473	6	4.4	261	2	Q7WFL6	Q7wfl6 bordetella
401	6	4.4	234	1	SNG1_RAT	Q62876 rattus norv	474	6	4.4	262	2	Q9RB26	Q9rb26 peptobacter
402	6	4.4	234	2	Q26747	Q26747 methanobact	475	6	4.4	262	2	Q9XB51	Q9xb51 erwinia car
403	6	4.4	235	2	Q662E2	Q662e2 borrelia ga	476	6	4.4	262	2	Q6CZM8	Q6czm8 erwinia car
404	6	4.4	235	2	Q92KY7	Q92ky7 rhizobium m	477	6	4.4	263	2	Q6NJH0	Q6njh0 corynebacte
405	6	4.4	236	2	Q82WR9	Q8zwr9 pyrobaculum	478	6	4.4	264	2	O87202	O87202 azospirillum
406	6	4.4	236	2	Q82ZB2	Q82zb2 enterococcu	479	6	4.4	264	2	O9HZV7	O9hzt7 pseudomonas
407	6	4.4	239	2	Q987U4	Q987u4 rhizobium 1	480	6	4.4	265	2	Q7QQF8	Q7qqf8 giardia lam
408	6	4.4	239	2	O8D2M8	O8d2m8 wiggleswort	481	6	4.4	265	2	O8RPD5	O8rpd5 legionella
409	6	4.4	239	2	Q9KFK5	Q9kfk5 bacillus ha	482	6	4.4	265	2	Q9PDK8	Q9fdk8 zymomonas m
410	6	4.4	240	2	O30144	O30144 archaeoglob	483	6	4.4	265	2	Q7V3Z4	Q7v3z4 prochloroco
411	6	4.4	240	2	Q6NCC7	Q6ncc7 rhodospseudo	484	6	4.4	266	2	Q7VNX0	Q7vnx0 haemophilus
412	6	4.4	242	2	Q81JV6	Q81jv6 plasmodium	485	6	4.4	266	2	O6DC54	O6dc54 brachydanio
413	6	4.4	242	2	Q7Z0H0	Q7z0h0 plasmodium	486	6	4.4	267	2	O6CLX9	O6clx9 kluyveromyc
414	6	4.4	242	2	Q82RL6	Q82rl6 streptomyc	487	6	4.4	268	1	ET1B_XENLA	P18756 xenopus lae
415	6	4.4	242	2	Q6AKI2	Q6aki2 desulfotale	488	6	4.4	268	2	Q8I6J7	Q8i6j7 ciona intes
416	6	4.4	242	2	Q8BFF7	Q8bf77 uncultured	489	6	4.4	269	2	Q9W4X7	Q9w4x7 rosophilla
417	6	4.4	242	2	Q6RXJ0	Q6rxj0 human cytom	490	6	4.4	269	2	Q74PA9	Q74pa9 yersinia pe
418	6	4.4	242	2	Q75RX5	Q75rx5 oreochromis	491	6	4.4	269	2	O8YBG1	O8ybg1 brucella me
419	6	4.4	243	2	O6INE4	Q6ine4 xenopus lae	492	6	4.4	269	2	O8YFH2	O8yfh2 bradyrhizob
420	6	4.4	244	2	Q8WQY9	Q8wqy9 aphrocalis	493	6	4.4	269	2	O8CZF9	O8czf9 yersinia pe
421	6	4.4	244	2	Q74K22	Q74kz2 lactobacill	494	6	4.4	269	2	Q8FWY4	Q8fwy4 brucella su
422	6	4.4	245	2	Q8Y189	Q8y189 raistonia s	495	6	4.4	270	2	Q74DN6	Q74dn6 geobacter s
423	6	4.4	245	2	Q88I43	Q88i43 pseudomonas	496	6	4.4	271	2	P78731	P78731 pneumocysti
424	6	4.4	246	2	O61WQ4	O61wq4 burkholderi	497	6	4.4	272	2	Q9Y7L38	Q9y7l38 clostridium
425	6	4.4	246	2	Q9SY37	Q9sy37 arabidopsis	498	6	4.4	273	2	O91G96	O91g96 columbid ci
426	6	4.4	246	2	Q8RGB2	Q8rgb2 fusobacteri	499	6	4.4	273	2	O91GA1	O91ga1 columbid ci
427	6	4.4	246	2	O6NGD2	Q6ngd2 corynebacte	500	6	4.4	273	2	Q9IG42	Q9ig42 columbid ci
428	6	4.4	246	2	Q9NFV3	Q9nfv3 gloeobacter	501	6	4.4	274	1	GADX_ECO27	Q9eyv5 escherichia
429	6	4.4	247	1	Y125_RICPR	P41087 rickettsia	502	6	4.4	274	1	GADX_ECO57	P58230 escherichia
430	6	4.4	247	1	Y167_RICCN	Q92ja0 rickettsia	503	6	4.4	274	1	GADX_ECOL6	Q8fcf6 escherichia
431	6	4.4	247	2	Q7PAR7	Q7par7 rickettsia	504	6	4.4	274	1	GADX_ECOL6	P37639 escherichia
432	6	4.4	247	2	O8PPL6	O8ppl6 xanthomonas	505	6	4.4	274	1	GADX_SHIFL	O83pr0 shigella fl
433	6	4.4	247	2	O68XP2	O68xp2 rickettsia	506	6	4.4	274	1	THCF_RHOER	O05691 rhodococcus
434	6	4.4	247	2	Q9KFL0	Q9kfl0 bacillus ha	507	6	4.4	275	2	Q6MLJ97	Q6mlj97 bdellovibri
435	6	4.4	247	2	Q8BF96	Q8bf96 uncultured	508	6	4.4	275	2	O9CCW0	Q9ccw0 mycobacteri
436	6	4.4	248	1	GRPE_ANASP	Q9yua7 anabaena sp	509	6	4.4	276	2	Q6Z9X5	Q6z9x5 oryza sativ
437	6	4.4	248	2	Q95438	Q95438 pseudomonas	510	6	4.4	276	2	Q737L6	Q737l6 bacillus ce
438	6	4.4	248	2	Q73ECO	Q73ec0 bacillus ce	511	6	4.4	277	2	O86ZC6	O86zc6 gibberella
439	6	4.4	248	2	Q91314	Q91314 pseudomonas	512	6	4.4	277	2	O53640	O53640 streptococc
440	6	4.4	249	2	Q6D4F3	Q6d4p3 erwinia car	513	6	4.4	277	2	Q887P6	Q887p6 pseudomonas
441	6	4.4	249	2	Q8UJS0	Q8ujs0 agrobacteri	514	6	4.4	277	2	Q8DYF6	Q8dyf6 streptococc
442	6	4.4	250	2	Q636V7	Q636v7 bacillus ce	515	6	4.4	277	2	O8DZN3	O8dzn3 streptococc
443	6	4.4	250	2	Q9YMY8	Q9ymy8 anabaena sp	516	6	4.4	277	2	O8FPY2	O8fpv2 corynebacte
444	6	4.4	250	2	Q733B4	Q733b4 bacillus ce	517	6	4.4	278	1	BMRR_BACSU	P39075 bacillus su
445	6	4.4	250	2	O81A69	Q81a69 bacillus ce	518	6	4.4	278	2	O64773	O64773 arabidopsis
446	6	4.4	250	2	Q81WM6	Q81wm6 bacillus an	519	6	4.4	278	2	Q40768	Q40768 prunus dulc
447	6	4.4	250	2	Q6HF92	Q6hf92 bacillus th	520	6	4.4	280	2	O8PI45	O8pi45 xanthomonas
448	6	4.4	251	2	Q663S0	Q663s0 yersinia ps	521	6	4.4	281	2	O64NU1	O64nu1 bacteroides
449	6	4.4	251	2	Q8Z9T6	Q8z9t6 yersinia pe	522	6	4.4	282	2	O8TJZ1	O8tjz1 methanosarc
450	6	4.4	252	2	Q7P501	Q7p501 fusobacteri	523	6	4.4	282	2	Q74BQ6	Q74bq6 geobacter s
451	6	4.4	252	2	Q8RH62	Q8rh62 fusobacteri	524	6	4.4	283	2	Q9AA26	Q9aa26 caulobacter
452	6	4.4	253	2	Q7YU2	Q7yu2 sulfolobus	525	6	4.4	285	2	Q97UF4	Q97uf4 sulfolobus
453	6	4.4	253	2	Q70MM8	Q70mm8 crassostrea	526	6	4.4	286	2	O53710	O53710 mycobacteri
454	6	4.4	254	2	Q9UF65	Q9uf65 homo sapien	527	6	4.4	286	2	Q7U252	Q7u252 mycobacteri
455	6	4.4	255	2	P78727	P78727 pneumocysti	528	6	4.4	286	2	Q9K7Q6	Q9k7q6 bacillus ha
456	6	4.4	255	2	O6NLM6	O6nlm6 drosophila	529	6	4.4	287	2	O6TMY7	O6tmv7 hyphomonas
457	6	4.4	255	2	O68049	O68049 rhodobacter	530	6	4.4	287	2	Q8PNB7	Q8pnb7 xanthomonas
458	6	4.4	255	2	Q88NR7	Q88nr7 pseudomonas	531	6	4.4	287	2	Q9CHQ9	Q9chq9 lactococcus
459	6	4.4	256	2	Q95Z09	Q95z09 trypanosoma	532	6	4.4	287	2	Q6DFS0	Q6dfs0 xenopus tro
460	6	4.4	256	2	Q7PE56	Q7pe56 anopheles g	533	6	4.4	288	2	Q9XUZ4	Q9xuz4 caenorhabdi
461	6	4.4	256	2	Q9DXH5	Q9dxh5 tomato spot	534	6	4.4	289	2	O8YSU1	O8ysu1 anabaena sp
462	6	4.4	257	1	DLHH_SULSO	P95862 sulfolobus	535	6	4.4	289	2	Q9J5E0	Q9j5e0 fowlpox vir
463	6	4.4	257	2	Q8FY43	Q8fy43 brucella su	536	6	4.4	290	1	EX05_BPT5	P06229 bacterioph
464	6	4.4	258	2	Q92KZ5	Q92kz5 rhizobium m	537	6	4.4	291	1	Y620_METJA	P06293 methanococc
465	6	4.4	260	2	Q6BQC2	Q6bqc2 debaryomyce	538	6	4.4	292	1	MDCB_ACICA	Q58m37 methanococc
466	6	4.4	260	2	Q7VM79	Q7vm79 haemophilus	539	6	4.4	292	2	O8LAG0	O8lag0 arabidopsis
467	6	4.4	261	2	Q96XK4	Q96xk4 sulfolobus	540	6	4.4	292	2	Q9FWT1	Q9fw1 arabidopsis
468	6	4.4	261	2	P78729	P78729 pneumocysti	541	6	4.4	292	2	Q9FY94	Q9fy94 arabidopsis
469	6	4.4	261	2	Q94YM6	Q94ym6 rana nigrom	542	6	4.4	293	1	YFIE_ECOLI	P33634 escherichia

543	6	4.4	293	2	Q72JW2	Q72jw2 thermus the	616	6	4.4	315	2	Q6E298	Q6e298 arabidopsis
544	6	4.4	294	2	Q94E53	Q94e53 oryza sativ	617	6	4.4	315	2	Q9FX92	Q9fx92 arabidopsis
545	6	4.4	295	2	Q9FW23	Q9fw23 arabidopsis	618	6	4.4	315	2	Q8CNA0	Q8cna0 staphylococ
546	6	4.4	296	2	Q8P7C3	Q8p7c3 xanthomonas	619	6	4.4	316	2	O58654	O58654 pyrococcus
547	6	4.4	297	2	Q8P1P6	Q8p1p6 xanthomonas	620	6	4.4	316	2	O58VX4	O58vx4 manheimia
548	6	4.4	298	2	Q20811	Q20811 caenorhabdi	621	6	4.4	316	2	Q88121	Q88121 pseudomonas
549	6	4.4	299	2	Q8PAE8	Q8pae8 xanthomonas	622	6	4.4	316	2	Q9PNG1	Q9pn61 campylobact
550	6	4.4	300	2	Q8ECOS7	Q8e8os7 escherichia	623	6	4.4	317	2	Q738B9	Q738b9 bacillus ce
551	6	4.4	301	2	MALG_ECOL6	P68185 escherichia	624	6	4.4	318	2	Q7R9B3	Q7r9b3 plasmodium
552	6	4.4	302	2	MALG_ECOLI	P68184 escherichia	625	6	4.4	318	2	Q8GTW7	Q8gtw7 oryza sativ
553	6	4.4	303	2	MALG_ENTAB	P68183 escherichia	626	6	4.4	318	2	Q9RHT5	Q9rht5 streptomyce
554	6	4.4	304	2	MALG_PHOLL	P18814 enterobacte	627	6	4.4	318	2	Q82CH1	Q82ch1 streptomyce
555	6	4.4	305	2	MALG_SALTY	Q7n983 photorhabdu	628	6	4.4	318	2	Q89XX4	Q89xx4 bradyrhizob
556	6	4.4	306	2	MALG_SALTY	Q8z1u3 salmonella	629	6	4.4	318	2	Q9KVD3	Q9kvd3 vibrio chol
557	6	4.4	307	2	MALG_SHIFL	P26468 shigella fl	630	6	4.4	318	2	Q9PM73	Q9pm73 campylobact
558	6	4.4	308	2	O6CD51	Q6cd51 yarrowia li	631	6	4.4	319	2	O8S629	O8s629 oryza sativ
559	6	4.4	309	2	Q664X1	Q664x1 yersinia ps	632	6	4.4	319	2	Q83X38	Q83x38 streptomyce
560	6	4.4	310	2	Q7VIG3	Q7vig3 helicobacte	633	6	4.4	319	2	Q7MT26	Q7mt26 porphyromon
561	6	4.4	311	2	Q9A589	Q9a589 caulobacter	634	6	4.4	320	2	O06996	O06996 bacillus su
562	6	4.4	312	2	Q9HX00	Q9hx00 pseudomonas	635	6	4.4	320	2	Q97GF5	Q97gf5 clostridium
563	6	4.4	313	2	Q8OXY0	Q8oxy0 garlic late	636	6	4.4	320	2	Q73M86	Q73m86 treponema d
564	6	4.4	314	2	Q8UZA2	Q8uza2 garlic late	637	6	4.4	321	2	O67QA9	O67qa9 symbiobacte
565	6	4.4	315	2	Q8X121	Q8x121 pneumocysti	638	6	4.4	321	2	Q986M3	Q986m3 rhizobium l
566	6	4.4	316	2	Q8ZMX6	Q8zmx6 salmonella	639	6	4.4	321	2	Q8R310	Q8r310 mus musculu
567	6	4.4	317	2	Q7MR96	Q7mr96 wolinnella s	640	6	4.4	322	2	Q983C4	Q983c4 rhizobium l
568	6	4.4	318	2	Q7D9X3	Q7vdj3 drosophila	641	6	4.4	322	2	Q8JFW6	Q8jfw6 brachydanio
569	6	4.4	319	2	Q7D9X3	Q7d9x3 mycobacteri	642	6	4.4	323	2	O6KZU0	O6kzu0 picrophilus
570	6	4.4	320	2	P96811	P96811 mycobacteri	643	6	4.4	323	2	O650S2	O650s2 bacteroides
571	6	4.4	321	2	Q8ARY6	Q8ary6 desulfotale	644	6	4.4	323	2	Q89XV0	Q89xv0 bradyrhizob
572	6	4.4	322	2	Q9E7N7	Q9e7n7 lettuce nec	645	6	4.4	324	2	Q9UUP4	Q9uup4 pneumocysti
573	6	4.4	323	2	O26437	O26437 methanobact	646	6	4.4	324	2	Q738W6	Q738w6 bacillus ce
574	6	4.4	324	2	Q65H73	Q65h73 bacillus li	647	6	4.4	324	2	Q81RL2	Q81rl2 bacillus an
575	6	4.4	325	2	Q89PG1	Q89pg1 bradyrhizob	648	6	4.4	324	2	O6HJB5	O6hjb5 bacillus th
576	6	4.4	326	2	MALG_YERPE	Q74rf8 yersinia pe	649	6	4.4	325	2	O7VZT6	O7vzt6 bordetella
577	6	4.4	327	2	Q8EUG3	Q8eug3 oryza sativ	650	6	4.4	325	2	Q7WS74	Q7ws74 bordetella
578	6	4.4	328	2	Q8PLN1	Q8pln1 xanthomonas	651	6	4.4	325	2	Q7WCQ4	Q7wcq4 bordetella
579	6	4.4	329	2	Q9K3X6	Q9k3x6 streptomyce	652	6	4.4	325	2	Q7ZZ64	Q7zz64 brachydanio
580	6	4.4	330	2	Q7ZZ63	Q7zz63 brachydanio	653	6	4.4	326	1	VP40_EBOZM	Q00030 equine herp
581	6	4.4	331	2	Q8EIN6	Q8ein6 shewanella	654	6	4.4	326	2	Q92Z59	Q92z59 rhizobium m
582	6	4.4	332	2	FMT_CAMJE	Q9pj28 campylobact	655	6	4.4	326	2	Q81DZ5	Q81dz5 bacillus ce
583	6	4.4	333	2	P72579	P72579 sulfolobus	656	6	4.4	326	2	Q82DK7	Q82dk7 streptomyce
584	6	4.4	334	2	Q86Y68	Q86y68 sulfolobus	657	6	4.4	326	2	Q39251	Q39251 equid herpe
585	6	4.4	335	2	O32796	Q32796 lactococcus	658	6	4.4	326	2	Q913A4	Q913a4 zaire ebola
586	6	4.4	336	2	O32798	Q32798 lactococcus	659	6	4.4	326	2	Q913A4	Q913a4 zaire ebola
587	6	4.4	337	2	Q7ND98	Q7nd98 gloeobacter	660	6	4.4	327	2	Q9M6R7	Q9m6r7 psium sativ
588	6	4.4	338	2	Q835V5	Q835v5 enterococcu	661	6	4.4	327	2	Q8UJL3	Q8ujl3 agrobacteri
589	6	4.4	339	2	EXTN_DAUCA	Q91259 streptomyce	662	6	4.4	328	1	ABF2_STRCK	P82594 streptomyce
590	6	4.4	340	2	EXTN_DAUCA	P06599 daucus caro	663	6	4.4	328	1	NC5R_ARATH	P83291 arabidopsis
591	6	4.4	341	2	YMC1_YEAST	P32331 saccharomyc	664	6	4.4	328	2	Q9D7H2	Q9d7h2 mus musculu
592	6	4.4	342	2	Q61QC7	Q61qc7 brachydanio	665	6	4.4	329	2	O18071	O18071 caenorhabdi
593	6	4.4	343	2	Q8FF12	Q8ff12 escherichia	666	6	4.4	329	2	Q9MPE7	Q9mfe7 beta vulgar
594	6	4.4	344	2	Q83Q11	Q83q11 shigella fl	667	6	4.4	329	2	Q92TI6	Q92ti6 rhizobium m
595	6	4.4	345	2	Q8X5A8	Q8x5a8 escherichia	668	6	4.4	329	2	Q80PX1	Q80px1 human herpe
596	6	4.4	346	2	Q96EJ8	Q96ej8 homo sapien	669	6	4.4	329	2	Q80PX2	Q80px2 human herpe
597	6	4.4	347	2	Q86X20	Q86x20 homo sapien	670	6	4.4	329	2	Q80PX3	Q80px3 human herpe
598	6	4.4	348	2	Q7MP27	Q7mp27 vibrio vuln	671	6	4.4	329	2	Q80PX4	Q80px4 human herpe
599	6	4.4	349	2	Q7NOA8	Q7noa8 photorhabdu	672	6	4.4	329	2	Q80PX5	Q80px5 human herpe
600	6	4.4	350	2	CNJC_TETTH	P16925 tetrahymena	673	6	4.4	330	2	Q76852	Q76852 tetrahymena
601	6	4.4	351	2	P96562	P96562 amycollatops	674	6	4.4	330	2	Q41402	Q41402 sebania ro
602	6	4.4	352	2	O44984	O44984 caenorhabdi	675	6	4.4	331	1	LDHD_LEUMC	P51011 leuconostoc
603	6	4.4	353	2	Q87UM8	Q87um8 pseudomonas	676	6	4.4	331	2	O6ZFU6	O6zfu6 oryza sativ
604	6	4.4	354	2	Y531_METTH	O26631 methanobact	677	6	4.4	331	2	O83359	O83359 treponema p
605	6	4.4	355	2	Q817L1	Q817l1 listeria mo	678	6	4.4	331	2	Q9JIT7	Q9jit7 cavia porce
606	6	4.4	356	2	Q720F6	Q720f6 listeria mo	679	6	4.4	331	2	Q8JXP9	Q8jpx9 reston ebol
607	6	4.4	357	2	Q895S8	Q895s8 clostridium	680	6	4.4	332	2	Q96ZS5	Q96z55 sulfolobus
608	6	4.4	358	2	Q25523	Q25523 helicobacte	681	6	4.4	332	2	Q84I39	Q84i39 helicobacte
609	6	4.4	359	2	Q8Y556	Q8y556 listeria mo	682	6	4.4	332	2	Q6M9Z5	Q6m9z5 paracchlamyd
610	6	4.4	360	2	Q71XE5	Q71xe5 listeria mo	683	6	4.4	333	2	O81494	O81494 arabidopsis
611	6	4.4	361	2	Q9KA02	Q9ka02 bacillus ha	684	6	4.4	333	2	Q87GK7	Q87gy7 vibrio para
612	6	4.4	362	2	Q92KZ4	Q92kz4 helicobacte	685	6	4.4	333	2	Q9JS73	Q9js73 chlamydia p
613	6	4.4	363	2	HEM3_BRUME	Q8yjb0 bruceella me	686	6	4.4	333	2	Q926L1	Q926l1 chlamydia p
614	6	4.4	364	2	HEM3_BRUME	Q8yjb0 bruceella me	687	6	4.4	334	1	PURR_PASMU	Q9cn88 pasteurella
615	6	4.4	365	2	HEM3_BRUME	Q8yjb0 bruceella me	688	6	4.4	334	1		

689	6	4.4	334	2	O45307	O45307 caenorhabdi	762	6	4.4	358	2	O6UDM3	O6udm3 psittacid h
690	6	4.4	335	2	Q9UZM6	Q9uzm6 pyrococcus	763	6	4.4	359	1	AROB_CHRVO	Q7nzu4 chromobacte
691	6	4.4	336	2	Q7PWN4	Q7pwn4 anopheles g	764	6	4.4	359	1	HFE_MOUSE	Q70387 mus musculu
692	6	4.4	335	1	XRC4_HUMAN	Q13426 homo sapien	765	6	4.4	359	2	O6N3V1	Q6n3v1 rhodopsueto
693	6	4.4	336	2	Q67MQ8	Q67mq8 symbiobacte	766	6	4.4	359	2	O8EYI5	O8eyi5 leptospira
694	6	4.4	336	2	Q84I37	Q84i37 heliobacte	767	6	4.4	359	2	O9D754	O9d754 mus musculu
695	6	4.4	337	2	O58840	O58840 pyrococcus	768	6	4.4	361	2	O8T376	O8t376 meloidogyne
696	6	4.4	337	2	Q8U204	Q8u204 pyrococcus	769	6	4.4	362	1	ASG2_YEAST	P11163 saccharomyc
697	6	4.4	337	2	Q75LX7	Q75lx7 oryza sativ	770	6	4.4	362	2	O6Q5K8	O6q5k8 saccharomyc
698	6	4.4	337	2	Q84I35	Q84i35 heliobacte	771	6	4.4	362	2	O6Q5K9	O6q5k9 saccharomyc
699	6	4.4	337	2	Q73XD2	Q73xd2 mycobacteri	772	6	4.4	362	2	O7AH88	O7ah88 escherichia
700	6	4.4	337	2	Q89GY5	Q89gy5 bradyrhizob	773	6	4.4	362	2	O6F7E5	O6f7e5 acinetobact
701	6	4.4	339	2	O7MXV9	Q7mxy9 porphyromon	774	6	4.4	363	2	Q9NVL6	Q9nvl6 homo sapien
702	6	4.4	339	2	Q6VZQ0	Q6vzq0 canarypox v	775	6	4.4	363	2	Q9RKQ5	Q9rkq5 streptomyce
703	6	4.4	340	2	Q6C875	Q6c875 yarrowia li	776	6	4.4	364	2	O6A6V5	O6a6v5 propionibac
704	6	4.4	340	2	Q69J25	Q69j25 oryza sativ	777	6	4.4	365	1	AROB_PSPFK	Q88cv2 pseudomonas
705	6	4.4	340	2	Q8ABQ4	Q8abq4 bacteroides	778	6	4.4	365	2	O8X6B9	O8x6b9 escherichia
706	6	4.4	340	2	O6YCH1	Q6ych1 mus musculu	779	6	4.4	365	2	O87v15	O87v15 pseudomonas
707	6	4.4	341	2	O8LMT1	Q8lmt1 arabidopsis	780	6	4.4	367	2	O6RCI2	Q6rci2 mycobacteri
708	6	4.4	341	2	Q8MPL1	Q8mpl1 bdellovibri	781	6	4.4	367	2	Q7MVZ4	Q7mvz4 porphyromon
709	6	4.4	341	2	Q7T5J0	Q7t5j0 cryptophleb	782	6	4.4	367	2	O6ZQ44	Q6zq44 mus musculu
710	6	4.4	342	2	Q93KV2	Q93kv2 streptomyce	783	6	4.4	368	1	AROB_PSEAE	P34002 pseudomonas
711	6	4.4	342	2	Q66IY2	Q66iy2 xenopus lae	784	6	4.4	369	1	HI82_PSEAE	Q9hz68 pseudomonas
712	6	4.4	342	2	Q6DFO7	Q6dfq7 xenopus tro	785	6	4.4	369	2	O84I36	O84i36 heliobacte
713	6	4.4	343	2	Q84I34	Q84i34 heliobacte	786	6	4.4	369	2	O6NIM2	O6nim2 corynebacte
714	6	4.4	343	2	Q8Y4I4	Q8y4i4 listeria mo	787	6	4.4	370	1	HUPK_RHLIV	P28153 rhizobium l
715	6	4.4	343	2	Q927H6	Q927h6 listeria in	788	6	4.4	370	2	O6BRJ2	Q6brj2 debaryomyce
716	6	4.4	343	2	Q71WA8	Q71wa8 listeria mo	789	6	4.4	370	2	Q7Q057	Q7qq57 giardia lam
717	6	4.4	344	1	PILT_PSEAE	P24559 pseudomonas	790	6	4.4	370	2	O916T2	Q916t2 pseudomonas
718	6	4.4	344	2	Q7BTG5	Q7btg5 pseudomonas	791	6	4.4	371	2	O93NC0	Q93nc0 myxococcus
719	6	4.4	344	2	Q9F667	Q9f667 pseudomonas	792	6	4.4	371	2	O67JF5	O67jf5 symbiobacte
720	6	4.4	344	2	Q87CD4	Q87cd4 xylella fas	793	6	4.4	372	1	DNAJ_BACSU	P17631 bacillus su
721	6	4.4	344	2	Q87V94	Q87v94 pseudomonas	794	6	4.4	372	2	Q8YUA9	Q8yua9 anabaena sp
722	6	4.4	344	2	Q9PCX1	Q9pcx1 xylella fas	795	6	4.4	373	2	O8P402	Q8p402 xanthomonas
723	6	4.4	345	1	ADD_RALSO	Q8xxl5 ralstonia s	796	6	4.4	374	2	O9PTL7	Q9ptl7 xenopus lae
724	6	4.4	345	1	CYSA_VIBU	Q8d653 vibrio vuln	797	6	4.4	376	1	Y5D9_GLOVI	Q7ndu3 gloeobacter
725	6	4.4	345	1	VAOD_YEAST	P32366 saccharomyc	798	6	4.4	376	2	O9Y8P6	Q9y8p6 aeropyrum p
726	6	4.4	345	2	Q8NL23	Q8nl23 xanthomonas	799	6	4.4	376	2	Q7PQV5	Q7pqv5 anopheles g
727	6	4.4	345	2	Q7CLR1	Q7clr1 xanthomonas	800	6	4.4	376	2	O67L31	Q67l31 symbiobacte
728	6	4.4	345	2	Q7PLN4	Q7pln4 chromobacte	801	6	4.4	376	2	O6DSY0	Q6dsy0 erwinia car
729	6	4.4	346	1	LUXA_PHOPO	P24113 photobacter	802	6	4.4	376	2	O37387	Q37387 common chim
730	6	4.4	346	2	Q97ZH7	Q97zh7 sulfolobus	803	6	4.4	376	2	O80IS9	Q80is9 xenopus lae
731	6	4.4	346	2	Q7WP94	Q7wp94 bordetella	804	6	4.4	377	2	O8GHV5	Q8ghv5 pseudomonas
732	6	4.4	346	2	O89LP2	Q89lp2 bradyrhizob	805	6	4.4	378	1	FLIY_BACSU	P24073 bacillus su
733	6	4.4	346	2	Q9RWH8	Q9rwh8 deinococcus	806	6	4.4	378	2	Q7XZAO	Q7x2a0 pseudomonas
734	6	4.4	347	2	Q8ZSW1	Q8zsw1 pyrobaculum	807	6	4.4	380	2	O6CHZ1	Q6chz1 yarrowia li
735	6	4.4	347	2	Q756V5	Q756v5 ashbya goss	808	6	4.4	380	2	Q73R97	Q73r97 treponema d
736	6	4.4	347	2	Q8P334	Q8p334 xanthomonas	809	6	4.4	380	2	Q9K000	Q9k000 neisseria m
737	6	4.4	347	2	O8XV23	Q8xv23 ralstonia s	810	6	4.4	381	1	ARGE_BUCAI	P57155 buchera ap
738	6	4.4	347	2	Q8A6V2	Q8a6v2 propionibac	811	6	4.4	381	2	Q8BIM3	Q8bim3 mus musculu
739	6	4.4	347	2	Q72M10	Q72m10 leptospira	812	6	4.4	384	2	O6YZP9	Q6yzp9 oryza sativ
740	6	4.4	347	2	Q8A2H5	Q8a2h5 bacteroides	813	6	4.4	384	2	O9EX13	Q9ex13 streptomyce
741	6	4.4	349	2	O18110	O18110 caenorhabdi	814	6	4.4	386	1	ARGJ_CORDI	P62059 corynebacte
742	6	4.4	349	2	O86JV0	Q86jv0 dictyosteli	815	6	4.4	386	1	CUE1_HUMAN	Q9nmw3 homo sapien
743	6	4.4	350	2	O56302	Q56302 thermococcu	816	6	4.4	386	2	O7PK57	Q7pk57 anopheles g
744	6	4.4	350	2	Q9XUC5	Q9xuc5 caenorhabdi	817	6	4.4	386	2	O64094	O64094 bacterioph
745	6	4.4	350	2	O8LEX1	Q8lex1 arabidopsis	818	6	4.4	386	2	O31927	Q31927 bacillus su
746	6	4.4	350	2	Q93Z83	Q93z83 arabidopsis	819	6	4.4	386	2	O98JJ5	Q98jj5 rhizobium l
747	6	4.4	350	2	Q9STW1	Q9stn1 arabidopsis	820	6	4.4	386	2	O6FEJ4	O6fej4 acinetobact
748	6	4.4	350	2	Q9ZUB9	Q9zub9 arabidopsis	821	6	4.4	388	1	CUE1_MOUSE	O8r3v6 mus musculu
749	6	4.4	350	2	Q7UPP7	Q7upp7 rhodopirell	822	6	4.4	388	2	O8ZYV9	O8zyv9 pyrobaculum
750	6	4.4	351	2	O81493	O81493 arabidopsis	823	6	4.4	388	2	Q96Z16	Q96z16 sulfolobus
751	6	4.4	351	2	Q944K0	Q944k0 arabidopsis	824	6	4.4	388	2	O16881	O16881 caenorhabdi
752	6	4.4	352	1	CYAB_STIAU	P40138 stigmatella	825	6	4.4	388	2	O8KE01	O8ke01 chlorobium
753	6	4.4	352	2	Q6BGM5	Q6bmg5 debaryomyce	826	6	4.4	389	2	O6LWY7	Q6lyw7 methanococc
754	6	4.4	353	2	Q6ZOV7	Q6zov7 oryza sativ	827	6	4.4	389	2	O6N4F5	Q6n4f5 rhodopsueto
755	6	4.4	356	2	O84I38	Q84i38 heliobacte	828	6	4.4	389	2	O89IU8	O89iu8 bradyrhizob
756	6	4.4	356	2	O8NR93	Q8nr93 corynebacte	829	6	4.4	389	2	O8DJV0	O8djv0 synechococc
757	6	4.4	356	2	Q7NVJ9	Q7nvd9 chromobacte	830	6	4.4	390	2	Q22101	Q22101 caenorhabdi
758	6	4.4	357	2	P78930	P78930 schizosacch	831	6	4.4	391	1	PCL_ECTHA	P42516 ectothiorho
759	6	4.4	357	2	Q74FZ0	Q74fz0 geobacter s	832	6	4.4	391	2	Q7JNC6	Q7jnc6 dirosophila
760	6	4.4	357	2	Q9DF34	Q9df34 brachydanio	833	6	4.4	391	2	Q7QGY4	Q7qgy4 anopheles g
761	6	4.4	358	2	Q8C2A6	Q8c2a6 mus musculu	834	6	4.4	391	2	Q02690	Q02690 podospora a

835	6	4.4	391	2	Q8D5A1	Q8d5a1 vibrio vuln	908	6	4.4	419	2	Q73F05	Q73f05 bacillus ce
836	6	4.4	392	1	LXC1_YARLI	P41929 yarrowia li	909	6	4.4	419	2	Q8FQ06	Q8fq06 corynebacte
837	6	4.4	392	2	Q629Y0	Q629y0 oryza sativ	910	6	4.4	419	2	Q6HPU5	Q6hpj5 bacillus th
838	6	4.4	392	2	Q8GALO	Q8gal0 arthrobacte	911	6	4.4	420	2	Q8PVS6	Q8pvs6 methanosarc
839	6	4.4	393	2	Q7Y0Z8	Q7y0z8 lycopersico	912	6	4.4	420	2	Q6X813	Q6x813 homo sapien
840	6	4.4	393	2	Q8RR83	Q8rr83 acetobacter	913	6	4.4	420	2	Q86UN3	Q86un3 homo sapien
841	6	4.4	393	2	Q921D8	Q921d8 mus musculu	914	6	4.4	420	2	Q7WE84	Q7we84 bordetella
842	6	4.4	394	2	Q6M2Z0	Q6m2z0 methylocyst	915	6	4.4	420	2	Q83A86	Q83a86 coxiella bu
843	6	4.4	394	2	Q8REN6	Q8ren6 fusobacteri	916	6	4.4	420	2	Q6AET0	Q6aet0 leifsonia x
844	6	4.4	394	2	Q6A5K4	Q6a5k4 propionibac	917	6	4.4	421	2	Q9SX61	Q9sx61 arabidopsis
845	6	4.4	394	2	Q7VVV1	Q7vvv1 bordetella	918	6	4.4	422	1	PROA_NITEU	Q820i7 nitrosomona
846	6	4.4	394	2	Q7WKL9	Q7wkl9 bordetella	919	6	4.4	423	2	Q70IN2	Q70in2 pseudomonas
847	6	4.4	394	2	Q9KB99	Q9kb99 bacillus ha	920	6	4.4	423	2	Q63BU5	Q63bu5 bacillus ce
848	6	4.4	395	2	Q7XEG1	Q7xeg1 oryza sativ	921	6	4.4	424	2	Q6F735	Q6f735 acinetobact
849	6	4.4	395	2	Q6EVS8	Q6evs8 versinia ps	922	6	4.4	424	2	Q7UL99	Q7ul99 rhodopirell
850	6	4.4	395	2	Q9KZC2	Q9kzc2 streptomyce	923	6	4.4	425	2	Q76652	Q76652 caenorhabdi
851	6	4.4	396	2	Q8BJ17	Q8bj17 debaryomyce	924	6	4.4	425	2	Q6JT24	Q6jt24 ornithocton
852	6	4.4	397	2	Q9UAU3	Q9uau3 caenorhabdi	925	6	4.4	426	2	Q8NAB8	Q8nab8 homo sapien
853	6	4.4	398	2	Q978Z4	Q978z4 thermoplasm	926	6	4.4	429	1	MANA_CANGA	Q76iq2 candida gla
854	6	4.4	398	2	Q05765	Q05765 saccharomyc	927	6	4.4	429	2	Q8SS48	Q8ss48 encaphalito
855	6	4.4	398	2	Q63R97	Q63r97 burkholderi	928	6	4.4	430	2	Q97AH4	Q97ah4 thermoplasm
856	6	4.4	399	2	Q9HGN6	Q9hgn6 schizosacch	929	6	4.4	430	2	Q7ML61	Q7ml61 vibrio vuln
857	6	4.4	399	2	Q8L912	Q8l912 arabidopsis	930	6	4.4	430	2	Q8A5C0	Q8a5c0 bacteroides
858	6	4.4	399	2	Q9M9V4	Q9m9v4 arabidopsis	931	6	4.4	431	1	FAAA_EMENI	Q00770 emeritella
859	6	4.4	400	2	Q9GZHV	Q9gzhv caenorhabdi	932	6	4.4	431	2	Q7MTJ6	Q7mtj6 porphyronon
860	6	4.4	400	2	Q6N8Z6	Q6n8z6 rhodopsendo	933	6	4.4	431	2	Q7TU40	Q7tu40 prochloroco
861	6	4.4	400	2	Q73ND4	Q73nd4 treponema d	934	6	4.4	432	2	Q94C40	Q94c40 arabidopsis
862	6	4.4	400	2	Q6P6Q1	Q6p6q1 mus musculu	935	6	4.4	432	2	Q9X804	Q9x804 streptomyce
863	6	4.4	401	2	Q8B6E3	Q8b6e3 rhizobium l	936	6	4.4	433	1	HTR2_HALVA	Q42258 haloarcula
864	6	4.4	401	2	Q7U8J2	Q7u8j2 synecococc	937	6	4.4	433	2	Q8YNO2	Q8ynq2 anabaena sp
865	6	4.4	402	2	Q8KES4	Q8kes4 chlorobium	938	6	4.4	433	2	Q7V019	Q7v019 prochloroco
866	6	4.4	402	2	Q7V4M1	Q7v4m1 prochloroco	939	6	4.4	433	2	Q9A3S6	Q9a3s6 caulobacter
867	6	4.4	402	2	Q6D669	Q6d669 erwinia car	940	6	4.4	434	2	Q07364	Q07364 chlamydia t
868	6	4.4	402	2	Q9W5Z9	Q9w5z9 fugu rubrip	941	6	4.4	434	2	Q84099	Q84099 chlamydia t
869	6	4.4	403	2	Q742P6	Q742p6 mycobacteri	942	6	4.4	434	2	Q823F1	Q823f1 chlamydophi
870	6	4.4	404	2	Q7QY67	Q7qy67 giardia lam	943	6	4.4	434	2	Q9PKT9	Q9pkt9 chlamydia m
871	6	4.4	404	2	Q7MC72	Q7mc72 vibrio vuln	944	6	4.4	434	2	Q9Z8M2	Q9z8m2 chlamydia p
872	6	4.4	405	2	Q97ZT8	Q97zt8 sulfobolus	945	6	4.4	436	1	RSMB_PSBPK	Q88rr3 pseudomonas
873	6	4.4	405	2	Q9AXJ7	Q9axj7 medicago tr	946	6	4.4	436	2	Q68604	Q68604 brevibacter
874	6	4.4	406	1	C5C4_AMYOR	Q8rn03 amycolatops	947	6	4.4	438	1	ET1A_XENLA	Q86604 xenopus lae
875	6	4.4	406	2	Q94IES	Q94ies cyanidiosch	948	6	4.4	438	2	Q64CT2	Q64ct2 uncultured
876	6	4.4	407	2	Q6CQN8	Q6ccn8 kluiveromyc	949	6	4.4	438	2	Q50175	Q50175 mycobacteri
877	6	4.4	407	2	Q6NCV1	Q6ncv1 rhodopsendo	950	6	4.4	439	2	Q9V0P1	Q9v0p1 pyrococcus
878	6	4.4	409	2	Q7PSZ8	Q7psz8 anopheles g	951	6	4.4	439	2	Q872D8	Q872d8 neurospora
879	6	4.4	409	2	Q65ZT1	Q65zt1 borrelia ga	952	6	4.4	439	2	Q6DJL5	Q6djl5 xenopus lae
880	6	4.4	410	2	Q6JKT4	Q6jkt4 zoothermopsi	953	6	4.4	440	1	ETSL_MOUSE	Q27577 mus musculu
881	6	4.4	410	2	Q6JKT7	Q6jkt7 zoothermopsi	954	6	4.4	440	2	Q50114	Q50114 pyrococcus
882	6	4.4	410	2	Q9AHF3	Q9ahf3 lysobacter	955	6	4.4	440	2	Q8VKH9	Q8vkh9 mycobacteri
883	6	4.4	411	2	Q9YCT5	Q9yct5 aeropyrum p	956	6	4.4	440	2	Q8Y490	Q8y490 listeria mo
884	6	4.4	411	2	Q7PT10	Q7pt10 anopheles g	957	6	4.4	440	2	Q927S8	Q927s8 listeria in
885	6	4.4	411	2	Q7W783	Q7w783 bordetella	958	6	4.4	440	2	Q71WL4	Q71wl4 listeria mo
886	6	4.4	412	2	Q8N6E0	Q8ne60 homo sapien	959	6	4.4	440	2	Q8BVW8	Q8bv8 mus musculu
887	6	4.4	413	2	Q9HEJ0	Q9hej0 neurospora	960	6	4.4	441	1	ETSL_HUMAN	Q4921 homo sapien
888	6	4.4	413	2	Q9NAL6	Q9nal6 caenorhabdi	961	6	4.4	441	1	ETSL_RAT	Q4156 rattus norv
889	6	4.4	414	2	Q61PK3	Q61pk3 photobacter	962	6	4.4	441	1	ETSA_CHICK	Q3474 gallus gall
890	6	4.4	414	2	Q7V099	Q7v099 prochloroco	963	6	4.4	441	2	Q6FG54	Q6fg54 homo sapien
891	6	4.4	415	2	Q8LP50	Q8lp50 lunaria ann	964	6	4.4	441	2	Q6Q428	Q6q428 oryctolagus
892	6	4.4	415	2	Q8SGB2	Q8sgb2 uncultured	965	6	4.4	441	2	Q69408	Q69408 eubacterium
893	6	4.4	415	2	Q7W0P6	Q7w0p6 bordetella	966	6	4.4	441	2	Q85376	Q85376 proteus mir
894	6	4.4	415	2	Q7W3F8	Q7w3f8 bordetella	967	6	4.4	442	2	Q7S2Z3	Q7s2z3 neurospora
895	6	4.4	415	2	Q7WES8	Q7wes8 bordetella	968	6	4.4	442	2	Q8X7V2	Q8x7v2 escherichia
896	6	4.4	416	2	Q63H22	Q63h22 bacillus ce	969	6	4.4	444	2	Q937R7	Q937r7 brucella me
897	6	4.4	416	2	Q811Y9	Q81iy9 bacillus ce	970	6	4.4	444	2	Q7MHR0	Q7mh0 vibrio vuln
898	6	4.4	416	2	Q81VL5	Q81vl5 bacillus an	971	6	4.4	444	2	Q8DCJ8	Q8dcj8 vibrio vuln
899	6	4.4	416	2	Q8DSQ3	Q8dsq3 streptococc	972	6	4.4	444	2	Q8FWL7	Q8fwl7 brucella su
900	6	4.4	417	2	Q6RC07	Q6rc07 mycobacteri	973	6	4.4	444	2	Q9HUR0	Q9hur0 pseudomonas
901	6	4.4	418	2	Q64NZ1	Q64nz1 bacteroides	974	6	4.4	445	2	Q6PCB0	Q6pcb0 homo sapien
902	6	4.4	418	2	Q91GF4	Q91gf4 epiphyas po	975	6	4.4	445	2	Q87YJ5	Q87yj5 pseudomonas
903	6	4.4	418	2	Q90ZA4	Q90za4 anbyetoma m	976	6	4.4	446	2	Q8A514	Q8a514 bacteroides
904	6	4.4	419	2	Q84DI2	Q84di2 caulobacter	977	6	4.4	446	2	Q9RSE8	Q9rse8 deinococcus
905	6	4.4	419	2	Q84D15	Q84di5 caulobacter	978	6	4.4	447	2	Q8SYV3	Q8syv3 dirosophila
906	6	4.4	419	2	Q84D18	Q84di8 caulobacter	979	6	4.4	447	2	Q75NB6	Q75nb6 pinctada fu
907	6	4.4	419	2	Q84DJ5	Q84dj5 caulobacter	980	6	4.4	447	2	Q64YV0	Q64yv0 bacteroides

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981 6 4.4 447 2 Q88113 pseudomonas
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983 6 4.4 448 2 Q63QB3 burkholderi
984 6 4.4 448 2 Q8XRUI ralstonia s
985 6 4.4 448 2 Q8G4D5 bifidobacte
986 6 4.4 449 2 Q5V0K4 mycobacteri
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988 6 4.4 450 2 Q8SS74 mus musculu
989 6 4.4 450 2 Q9PFM2 campylobact
990 6 4.4 452 2 Q7S1H7 neurospora
991 6 4.4 452 2 Q876W2 gibberella
992 6 4.4 452 2 Q876X4 fusarium sp
993 6 4.4 452 2 Q87BF5 xylella fas
994 6 4.4 452 2 Q8CXW1 escherichia
995 6 4.4 452 2 Q9PFT3 xylella fas
996 6 4.4 453 1 GR55 RAT
997 6 4.4 453 2 Q9PQK6 rattus norv
998 6 4.4 454 1 MURP SYN3
999 6 4.4 454 2 Q9LNH7 synecocyst
1000 6 4.4 454 2 Q93JA4 arabidopsis
Q93JA4 streptomyce
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ALIGNMENTS

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RESULT 1
Q723B6 PRELIMINARY; PRT; 803 AA.
AC Q723B6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein DKFZp686E1430.
GN Name=DKFZp686E1430;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human testis;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wienann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537955; CAD97922.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR InterPro; IPR003649; Bbox C.
DR InterPro; IPR002083; MATH_
DR InterPro; IPR009061; Putativ DNA_bind.
DR InterPro; IPR011054; Rndmt_hyb_motif.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50144; MATH; 1.
KW Hypothetical protein.
SQ SEQUENCE 803 AA; 89186 MW; 43486E1064478477 CRC64;

Query Match 100.0%; Score 135; DB 2; Length 803;
Best Local Similarity 100.0%; Pred. No. 5,1e-136;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVNGVGRGYLSVFL 60
Db 149 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVNGVGRGYLSVFL 208

Qy 61 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIEEFASDEVGECWGNVRFRLDLLANEGYL 120
Db 209 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIEEFASDEVGECWGNVRFRLDLLANEGYL 268

Qy 121 NPQNDTVILRFQVRS 135
Db 269 NPQNDTVILRFQVRS 283
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RESULT 2

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Q81YF7 PRELIMINARY; PRT; 964 AA.
AC Q81YF7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein DKFZp686E1430.
GN Name=DKFZp686E1430;
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OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036012; AAH36012.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH_
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 964 AA; 107875 MW; BD3E9177535EB9D CRC64;
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Query Match 100.0%; Score 135; DB 2; Length 964;

Best Local Similarity 100.0%; Pred. No. 6e-136;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVNGVGRGYLSVFL 60

Db 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVNGVGRGYLSVFL 330

```
Qy 61 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREPASDFEVCWCYGNRFFRLDLLANEGYL 120
Db 331 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREPASDFEVCWCYGNRFFRLDLLANEGYL 390

Qy 121 NPQNDTVILRFQVRS 135
Db 391 NPQNDTVILRFQVRS 405

RESULT 3
Q8WYF7 PRELIMINARY; PRT; 964 AA.
AC Q8WYF7
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE POB1
GN Name=POB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu G., Couch F.J.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF213365; AAL36460.1;
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF00643; zf-B_box; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00502; BBC; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00061; MATH; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50144; MATH; 1.
DR PROSITE: PS50119; ZF_BBOX; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 964 AA; 107861 MW; 76E5BA4C7901916D CRC64;

Query Match 100.0%; Score 135; DB 2; Length 964;
Best Local Similarity 100.0%; Pred. No. 6e-136;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVGVYLSVPLE 60
Db 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVGVYLSVPLE 330

Qy 61 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREPASDFEVCWCYGNRFFRLDLLANEGYL 120
Db 331 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREPASDFEVCWCYGNRFFRLDLLANEGYL 390

Qy 121 NPQNDTVILRFQVRS 135
Db 391 NPQNDTVILRFQVRS 405

RESULT 4
Q94972 PRELIMINARY; PRT; 979 AA.
AC Q94972
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE KIAA0998 protein (Fragment).
GN Name=KIAA0998;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hiroseawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RL for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMBL: AB020705; BAA74921.1; -.
DR Genew; HGNC:7523; TRIM37.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR003649; Bbox_C.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR008974; Traf_like.
DR InterPro: IPR000315; Znf_Box.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF00643; zf-B_box; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00502; BBC; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00061; MATH; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50144; MATH; 1.
DR PROSITE: PS50119; ZF_BBOX; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
FT NON TER 1
SQ SEQUENCE 979 AA; 109607 MW; D9958FE2EA23EEFD CRC64;

Query Match 100.0%; Score 135; DB 2; Length 979;
Best Local Similarity 100.0%; Pred. No. 6.1e-136;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVGVYLSVPLE 60
Db 286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVGVYLSVPLE 345

Qy 61 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREPASDFEVCWCYGNRFFRLDLLANEGYL 120
Db 346 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREPASDFEVCWCYGNRFFRLDLLANEGYL 405

Qy 121 NPQNDTVILRFQVRS 135
Db 406 NPQNDTVILRFQVRS 420

RESULT 5
Q8CHC5 PRELIMINARY; PRT; 928 AA.
AC Q8CHC5
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MKIAA0898 protein (Fragment).
GN Name=MKIAA0898;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RA Ohara O., Koga H.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB093271; BAC41455.1; -.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
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DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR000315; Znf_Bbox.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
DR NON_TER 1
SQ SEQUENCE 928 AA; 103732 MW; 23CEODAAD85BFDE CRC64;

Query Match 89.6%; Score 121; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 6.7e-121;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVGRGYLSVPLE 60
DB 238 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVGRGYLSVPLE 297

QY 61 LSAGLPETSKYEVYRVMVHQSCNDPTKNI IREFASDFEGVCWGYNFRFLDLLANEGYL 120
DB 298 LSAGLPETSKYEVYRVMVHQSCNDPTKNI IREFASDFEGVCWGYNFRFLDLLANEGYL 357

QY 121 N 121
DB 358 N 358

RESULT 6
Q6PCX9 ID Q6PCX9 PRELIMINARY; PRT; 961 AA.
AC Q6PCX9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tripartite motif protein 37.
GN Name=Trim37;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
```

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RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059070; AAH59070.1; -.
DR EMBL; BC058678; AAH58678.1; -.
DR GO; GO:0016015; F:morphogen activity; TAS.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR000315; Znf_Bbox.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 961 AA; 107659 MW; 85629CFE0A1D6EA CRC64;

Query Match 89.6%; Score 121; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 6.9e-121;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVGRGYLSVPLE 60
DB 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVGRGYLSVPLE 330

QY 61 LSAGLPETSKYEVYRVMVHQSCNDPTKNI IREFASDFEGVCWGYNFRFLDLLANEGYL 120
DB 331 LSAGLPETSKYEVYRVMVHQSCNDPTKNI IREFASDFEGVCWGYNFRFLDLLANEGYL 390

QY 121 N 121
DB 391 N 391

RESULT 7
Q95LM3 ID Q95LM3 PRELIMINARY; PRT; 721 AA.
AC Q95LM3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
RT in the human genome sequence.";
RL BMC Genomics 3:36-36(2002).
DR EMBL; AB071078; BAB64471.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR008974; Traf_like.
DR InterPro; IPR001841; Znf_Ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein_
SQ SEQUENCE 721 AA; 80131 MW; 203E974760F866E9 CRC64;
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Query Match          47.4%; Score 64; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 1.2e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 EYRVMHVSNDPTKNIIRFASDFEVEGCGYNNRFRRLDLLANEYLNPNQDVTILRF 131
    |||||
Db 100 EYRVMHVSNDPTKNIIRFASDFEVEGCGYNNRFRRLDLLANEYLNPNQDVTILRF 159

Qy 132 QVRS 135
    ||||
Db 160 QVRS 163

RESULT 8
G101_HUMAN
ID G101_HUMAN STANDARD; PRT; 508 AA.
AC Q96P66; Q8NG93;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable G protein-coupled receptor GPR101.
GN Name=GPR101;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0014-5793(02)00651-5;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
RA Takeda S., Kadowaki S., Haga T., Takasu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL FEBS Lett. 520:97-101(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF411115; AAL26486.1; --
DR EMBL; AB083588; BAB99301.1; --
DR EMBL; AB065937; BAC06152.1; ALT_INIT.
DR Genew; HGNC:14963; GPR101.
DR MIM; 300393; --
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 35 Extracellular (Potential).
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FT TRANSMEM 36 68 1 (Potential).
FT DOMAIN 57 68 Cytoplasmic (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT DOMAIN 90 106 Extracellular (Potential).
FT TRANSMEM 107 127 3 (Potential).
FT DOMAIN 128 149 Cytoplasmic (Potential).
FT TRANSMEM 150 170 4 (Potential).
FT DOMAIN 171 196 Extracellular (Potential).
FT TRANSMEM 197 217 5 (Potential).
FT DOMAIN 218 399 Cytoplasmic (Potential).
FT TRANSMEM 400 420 6 (Potential).
FT DOMAIN 421 433 Extracellular (Potential).
FT TRANSMEM 434 454 7 (Potential).
FT DOMAIN 455 508 Cytoplasmic (Potential).
FT DISULFID 104 182 By similarity.
FT CARBOHYD 7 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 13 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 508 AA; 56716 MW; E20A409F65C95B85 CRC64;

Query Match          6.7%; Score 9; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VPSYDSATF 11
    |||||
Db 499 VPSYDSATF 507

RESULT 9
O34947
ID O34947 PRELIMINARY; PRT; 210 AA.
AC O34947; Q79659;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Yoaz.
GN Name=Yoaz; OrderedLocusNames=BSU18790;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borrias R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Etian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.K., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kunano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maue C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadade Y., Sato I., Scanlan E., Schleich S., Schroter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serro P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenberg M., Vannier F.,
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RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yaumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
DR EMBL; AF027868; AAB84456.1; -.
DR EMBL; Z99114; CAB13771.1; -.
DR PIR; A69898; A69898.
DR InterPro; IPR002818; ThiJ/Pfpi.
DR Pfam; PF01965; DJ_1_Pfpi; 1.
KW Complete proteome.
SQ SEQUENCE 210 AA; 23420 MW; 19A8BA915AAEF745 CRC64;

Query Match 5.9%; Score 8; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 LANEGYLN 121
Db 116 LANEGYLN 123
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RESULT 10
Q65003 PRELIMINARY; PRT; 286 AA.
ID Q65003
AC Q65003;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative cell-to-cell movement protein.
OS Apple mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=12319;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95374352; PubMed=7646355;
RA Shiel P.J., Alrefai R.H., Domier L.L., Korban S.S., Berger P.H.;
RT "The complete nucleotide sequence of apple mosaic virus RNA-3.";
RL Arch. Virol. 140:1247-1256(1995).
DR EMBL; U15608; AAA86960.1; -.
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP; 1.
SQ SEQUENCE 286 AA; 32409 MW; D2A4493315A882C1 CRC64;

Query Match 5.9%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 SDFEVGEC 102
Db 10 SDFEVGEC 17
|||||

RESULT 11
Q63CU1 PRELIMINARY; PRT; 423 AA.
ID Q63CU1
AC Q63CU1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chlorohydrolase/deaminase family protein.
GN ORFNames=BTZK1681;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=286681;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ZK;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Longmire J., Lucas S., Okinaka R.,

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RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18572.1; -.
KW Hydrolase.
SQ SEQUENCE 423 AA; 46816 MW; BD583BC7F209A87B CRC64;

Query Match 5.9%; Score 8; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 EFASDFEV 99
Db 27 EFASDFEV 34
|||||

RESULT 12
Q81S14 PRELIMINARY; PRT; 435 AA.
ID Q81S14
AC Q81S14; Q61094; Q6KU68;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chlorohydrolase family protein.
GN OrderedLocusNames=BAL1865, BAS1729, GBAA1865;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Tourasse N.N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.B., Maumond Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.B., Niernan W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Kohler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Steirne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017030; AA825768.1; -.
DR EMBL; AE017334; AAT30980.2; -.
DR EMBL; AE017225; AAT54045.1; -.
DR HSPSP; Q9X034; 1P1M.
DR TIGR; BA1865; -.
DR TIGR; GBAA1865; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR011550; Amidohydro_1.
DR InterPro; IPR011059; Metallohydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD001248; Amidohydro_like; 1.

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KW Complete proteome; Hydrolase.
SQ SEQUENCE 435 AA; 48143 MW; 2D29289BAA5819B33 CRC64;

Query Match      5.9%; Score 8; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 EFASDFEV 99
DB 39 EFASDFEV 46
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RESULT 13
Q6HK87 PRELIMINARY; PRT; 435 AA.
AC Q6HK87;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Chlorohydrolase (deaminase family protein.
GN OrderedLocusNames=BT9727.1707;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Bretin T.S.; Bruce D.; Challacombe J.F.; Gilna P.; Han C.; Hill K.;
RA Hichcock P.; Jackson P.; Keim P.; Longmire J.; Lucas S.; Okinaka R.;
RA Richardson P.; Rubin E.; Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017355; AAT59611.1;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR011550; Amidohydro-like.
DR InterPro; IPR011059; Metallo hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD001248; Amidohydro like; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 435 AA; 48139 MW; 6BE505358AE3268 CRC64;

Query Match      5.9%; Score 8; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 EFASDFEV 99
DB 39 EFASDFEV 46
|||||

RESULT 14
Q8E8R3 PRELIMINARY; PRT; 1045 AA.
ID Q8E8R3;
AC Q8E8R3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heavy metal efflux pump, Czca family.
GN OrderedLocusNames=S04598;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F.; Paulsen I.T.; Nelson K.E.; Gaidos E.J.; Nelson W.C.;
RA Read T.D.; Eisen J.A.; Seshadri R.; Ward N.L.; Methe B.A.;
RA Clayton R.A.; Meyer T.; Tsapin A.; Scott J.; Beanan M.J.;
RA Brinkac L.M.; Daugherty S.C.; DeBoy R.T.; Dodson R.J.; Durkin A.S.;
RA Haft D.H.; Kolonay J.F.; Madupu R.; Peterson J.D.; Umayam L.A.;
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RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015891; AAN57558.1; -.
DR TIGR; S04598; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; P:cation transporter activity; IEA.
DR GO; GO:0006812; P:cation transporter; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR001036; Acrflavin_res.
DR InterPro; IPR004763; Czca.
DR Pfam; PF00873; Acr tran; 1.
DR PRINTS; PR00702; ACRIFLAVINRP.
DR TIGRFAMs; TIGR00914; 2A0601; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1045 AA; 114513 MW; 9E99187C3248C984 CRC64;

Query Match      5.9%; Score 8; DB 2; Length 1045;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 ELSAGLPE 67
DB 311 ELSAGLPE 318
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RESULT 15
Q89T67 PRELIMINARY; PRT; 98 AA.
ID Q89T67;
AC Q89T67;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bel2183 protein.
GN OrderedLocusNames=bel2183;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimp S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005942; BAC47448.1; -.
KW Complete proteome.
SQ SEQUENCE 98 AA; 10886 MW; 90279D1E01E99AD5 CRC64;

Query Match      5.2%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NDTVILR 130
DB 39 NDTVILR 45
|||||

Search completed: July 20, 2005, 20:52:18
Job time : 90.75 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:37:15 ; Search time 85.8 Seconds
(without alignments)
787.814 Million cell updates/sec

Title: US-09-706-325-24
Perfect score: 132
Sequence: 1 SYNTINNFSCREMGEVI.....EANGLLPDDKLTLPCEVSVV 132

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	373	2	Q76LV9 mus musculus
2	132	100.0	374	1	O43791 homo sapien
3	132	100.0	374	1	SPOP_MOUSE
4	132	100.0	374	2	Q8P8B3
5	132	100.0	374	2	Q7T330
6	132	100.0	374	2	Q7ZX06
7	132	100.0	425	2	Q9DBZ2
8	53	40.2	391	2	Q9HAB2
9	53	40.2	392	2	Q6IQ16
10	40	30.3	374	2	Q8MRB4
11	40	30.3	401	2	Q7PGC0
12	40	30.3	403	2	Q8ING4
13	40	30.3	406	2	Q7KSK6
14	40	30.3	451	1	VNV5_CAEEL
15	40	30.3	695	2	Q7PRD7
16	24	18.2	392	2	Q6GR09
17	9	6.8	364	2	Q717B2
18	9	6.8	365	2	Q717B4
19	9	6.8	417	2	Q22006
20	8	6.1	225	2	Q84ZC8
21	8	6.1	346	2	Q752C0
22	8	6.1	380	1	HYD1_BRAJA
23	8	6.1	496	2	Q33589
24	7	5.3	46	2	Q7RYV4
25	7	5.3	46	2	Q7A0E0
26	7	5.3	46	2	Q6G7S0
27	7	5.3	46	2	Q6GF35
28	7	5.3	60	2	Q83X46
29	7	5.3	67	2	Q7RU09
30	7	5.3	88	2	Q8VB68
31	7	5.3	91	2	Q7P610

32	7	5.3	91	2	Q8REL7	Q8rel7 fusobacteri
33	7	5.3	108	2	Q6CUQ4	Q6cuq4 kluveromyc
34	7	5.3	108	2	Q707Z2	Q707z2 kluveromyc
35	7	5.3	116	2	Q7X4T0	Q7x4t0 peanut wtc
36	7	5.3	136	1	FLIS_ECOLI	P26608 escherichia
37	7	5.3	136	2	Q9FKL7	Q9fkl7 arabidopsis
38	7	5.3	136	2	Q7AD05	Q7ad05 escherichia
39	7	5.3	136	2	Q8XBB7	Q8xbb7 escherichia
40	7	5.3	136	2	Q8FGM0	Q8fgm0 escherichia
41	7	5.3	136	2	Q83R42	Q83r42 shigella fl
42	7	5.3	143	2	Q58831	Q58831 pyrococcus
43	7	5.3	143	2	Q9KQK7	Q9kqk7 vibrio chol
44	7	5.3	156	2	Q8P5Z1	Q8p5z1 xanthomonas
45	7	5.3	160	2	Q9AVC4	Q9avc4 vallisenaria
46	7	5.3	172	2	Q8PH48	Q8pha8 xanthomonas
47	7	5.3	187	1	PTH_CHLTE	Q8kd05 chlorobium
48	7	5.3	191	2	Q6FJS6	Q6fjs6 candida gla
49	7	5.3	194	1	GRPE_LACAC	Q84bu5 lactobacill
50	7	5.3	197	2	Q9CK36	Q9ck36 pasteurella
51	7	5.3	204	2	Q6LKF0	Q6lko0 photobacter
52	7	5.3	205	2	Q8RYM7	Q8rym7 oryza sativ
53	7	5.3	207	2	Q7VXS4	Q7vxs4 bordetella
54	7	5.3	207	2	Q7W6Z7	Q7w6z7 bordetella
55	7	5.3	207	2	Q7WIV7	Q7wiv7 bordetella
56	7	5.3	213	2	Q8N3C9	Q8n3c9 homo sapien
57	7	5.3	217	2	Q97AQ7	Q97aq7 thermoplas
58	7	5.3	218	2	Q8C136	Q8c136 mus musculu
59	7	5.3	220	2	Q830M2	Q830m2 enterococcu
60	7	5.3	224	2	Q8CIJ8	Q8cij8 mus musculu
61	7	5.3	224	2	Q9QXH5	Q9qxh5 mus musculu
62	7	5.3	226	2	Q96B00	Q96b00 homo sapien
63	7	5.3	227	2	Q8NHE3	Q8nhe3 homo sapien
64	7	5.3	227	2	Q8TEL0	Q8tel0 homo sapien
65	7	5.3	231	2	Q9HM62	Q9hm62 thermoplas
66	7	5.3	241	1	GTOI_RAT	Q2z339 rattus norv
67	7	5.3	241	2	Q6AXR6	Q6axr6 rattus norv
68	7	5.3	259	2	Q6T8C8	Q6t8c8 helianthus
69	7	5.3	266	2	Q9DHR7	Q9dhr7 yaba-like d
70	7	5.3	296	1	KHSE_LACIA	Q9cgd7 lactococcus
71	7	5.3	296	1	KHSE_LACIC	P52991 lactococcus
72	7	5.3	298	1	Y5G0_ENCCU	Q8tj22 encephalito
73	7	5.3	298	2	Q8FMZ0	Q8fmz0 corynebacte
74	7	5.3	299	2	Q96603	Q96603 plodia inte
75	7	5.3	299	2	Q8GXS4	Q8gxs4 arabidopsis
76	7	5.3	302	2	Q97RX7	Q97rx7 streptococc
77	7	5.3	302	2	Q8FTU2	Q8ftu2 corynebacte
78	7	5.3	304	1	YBB1_BACSU	Q45582 bacillus su
79	7	5.3	310	2	Q9HVV1	Q9hvv1 pseudomonas
80	7	5.3	311	2	Q97ZS5	Q97zes sulfolobus
81	7	5.3	314	2	Q8SUP1	Q8sup1 encephalito
82	7	5.3	317	2	Q921J9	Q921j9 mus musculu
83	7	5.3	325	2	Q9M2I2	Q9m2i2 arabidopsis
84	7	5.3	331	1	RNZ_DEIRA	Q8rxp0 deinococcus
85	7	5.3	340	1	YI00_ARCFU	Q28474 archaeoglob
86	7	5.3	340	2	Q8G9H3	Q8g9h3 nitrospir
87	7	5.3	345	2	Q8KNY8	Q8kny8 helicobacte
88	7	5.3	345	2	Q7SLB3	Q7slb3 neurospora
89	7	5.3	353	2	Q6Z0V7	Q6z0v7 oryza sativ
90	7	5.3	353	2	Q8C8Y5	Q8c8y5 mus musculu
91	7	5.3	359	2	Q744A7	Q744a7 mycobacteri
92	7	5.3	361	2	Q8VI39	Q8vi39 mus musculu
93	7	5.3	365	2	Q717B3	Q717b3 mus musculu
94	7	5.3	365	2	Q71G58	Q71g58 mus musculu
95	7	5.3	365	2	Q8BZV7	Q8bzv7 mus musculu
96	7	5.3	370	2	Q6YCH2	Q6ych2 mus musculu
97	7	5.3	389	2	Q6R2D1	Q6r2d1 escherichia
98	7	5.3	401	2	Q9SUG5	Q9sug5 arabidopsis
99	7	5.3	421	1	FXJ1_HUMAN	Q92949 homo sapien
100	7	5.3	421	1	FXJ1_MOUSE	Q61660 mus musculu
101	7	5.3	421	1	FXJ1_RAT	Q63247 rattus norv
102	7	5.3	421	2	Q64Q08	Q64q08 mus musculu
103	7	5.3	440	2	Q73HT1	Q73ht1 wolbachia p
104	7	5.3	441	2	Q9SLB4	Q9slb4 arabidopsis

105	7	5.3	450	2	Q6LFR8	Q6lfr8 photobacter
106	7	5.3	459	2	Q9K440	Q9k440 streptomyce
107	7	5.3	461	2	Q8FL23	Q8fl23 corynebacte
108	7	5.3	470	2	Q6DVF9	Q6dvf9 podurea aqua
109	7	5.3	485	2	Q6QPL8	Q6qpl8 suaeda sald
110	7	5.3	506	2	Q9ACV6	Q9acv6 streptomyce
111	7	5.3	518	2	Q9KHA8	Q9kha8 synecococc
112	7	5.3	518	2	Q9JUA7	Q9jja7 mus musculu
113	7	5.3	520	2	Q96S94	Q96s94 homo sapien
114	7	5.3	563	1	Y963_METJA	Q58373 methanococc
115	7	5.3	567	1	PGTA_HUMAN	Q92696 homo sapien
116	7	5.3	567	1	PGTA_MOUSE	Q91bk4 mus musculu
117	7	5.3	567	1	PGTA_RAT	Q86602 rattus norv
118	7	5.3	567	2	Q8FHF7	Q8fhf7 homo sapien
119	7	5.3	569	2	Q6AN94	Q6an94 desulfotale
120	7	5.3	579	2	Q8BKT3	Q8bkt3 mus musculu
121	7	5.3	644	2	Q43994	Q43994 leishmania
122	7	5.3	644	2	Q8MNY9	Q8mny9 leishmania
123	7	5.3	644	2	Q70W26	Q70w26 leishmania
124	7	5.3	650	2	Q52870	Q52870 rhizobium l
125	7	5.3	657	1	GP63_LEITR	Q8mnz1 leishmania
126	7	5.3	657	2	Q70W25	Q70w25 leishmania
127	7	5.3	660	2	Q69710	Q69710 mycobacteri
128	7	5.3	660	2	Q7TVT0	Q7tvt0 mycobacteri
129	7	5.3	665	2	Q8BZP4	Q8bzp4 lactobacill
130	7	5.3	678	2	Q8BU31	Q8bu31 debaryomyce
131	7	5.3	684	2	Q8DQP2	Q8dqp2 streptococc
132	7	5.3	733	2	Q7QTS8	Q7qts8 giardia lam
133	7	5.3	745	1	C0PB_ENTHR	P05425 enterococcu
134	7	5.3	748	2	Q75JRO	Q75jro dictyosteli
135	7	5.3	773	2	Q3IMP3	Q3imp3 influenza c
136	7	5.3	774	1	RRP3_INCBE	P21770 influenza c
137	7	5.3	774	1	RRP3_INCUJ	P13877 influenza c
138	7	5.3	774	2	Q6I7C4	Q6i7c4 influenza c
139	7	5.3	774	2	Q82668	Q82668 influenza c
140	7	5.3	801	2	Q6WB34	Q6wb34 alcaligenes
141	7	5.3	817	2	P73619	P73619 synecocyst
142	7	5.3	844	2	Q9LE38	Q9le38 arabidopsis
143	7	5.3	860	2	Q75BV9	Q75bv9 ashbya goss
144	7	5.3	868	2	Q7NF67	Q7nf67 gloeobacter
145	7	5.3	1009	2	Q6P762	Q6p762 rattus norv
146	7	5.3	1013	1	M2B1_MOUSE	Q09159 mus musculu
147	7	5.3	1066	2	Q7XE90	Q7xe90 oryza sativ
148	7	5.3	1101	2	Q6CPW9	Q6cpw9 kluyveromyc
149	7	5.3	1122	2	Q43945	Q43945 leishmania
150	7	5.3	1293	2	Q9AXD6	Q9axd6 zea mays (m
151	7	5.3	2160	2	O17709	O17709 caenorhabdi
152	7	5.3	2248	2	Q7R5C1	Q7r5c1 giardia lam
153	7	5.3	2397	2	Q7SF97	Q7sf97 neurospora
154	7	5.3	3351	2	Q94907	Q94907 drosophila
155	7	5.3	3351	2	Q9V496	Q9v496 drosophila
156	6	4.5	20	2	Q9QVF9	Q9qvf9 rattus ep.
157	6	4.5	28	2	Q8K1D1	Q8k1d1 mus musculu
158	6	4.5	29	2	Q6EKK8	Q6ekk8 yersinia pe
159	6	4.5	40	2	Q6EKU1	Q6ekul yersinia pe
160	6	4.5	47	2	Q8FFI2	Q8ffl2 escherichia
161	6	4.5	50	2	Q6GZU6	Q6gzue frog virus
162	6	4.5	52	2	Q8ISR4	Q8isr4 spodoptera
163	6	4.5	53	2	Q8VKJ8	Q8vkj8 mycobacteri
164	6	4.5	55	2	Q7MI53	Q7mi53 vibrio vuln
165	6	4.5	56	2	Q9XHG5	Q9xhg5 arabidopsis
166	6	4.5	57	2	Q8CYA4	Q8cyaa streptococc
167	6	4.5	59	2	Q9WPH3	Q9wph3 equid herpe
168	6	4.5	60	2	Q8KEJ9	Q8kej9 chlorobium
169	6	4.5	60	2	Q96744	Q96744 feline herp
170	6	4.5	60	2	Q77VU7	Q77vu7 feline herp
171	6	4.5	60	2	Q77VU8	Q77vu8 feline herp
172	6	4.5	60	2	Q77VU9	Q77vu9 feline herp
173	6	4.5	60	2	Q77VV0	Q77vv0 feline herp
174	6	4.5	65	2	P87439	P87439 lepidodacty
175	6	4.5	65	2	P87440	P87440 lepidodacty
176	6	4.5	65	2	P87443	P87443 lepidodacty
177	6	4.5	65	2	P87449	P87449 lepidodacty

178	6	4.5	65	2	P87450	P87450 lepidodacty
179	6	4.5	65	2	P87451	P87451 lepidodacty
180	6	4.5	65	2	P87454	P87454 lepidodacty
181	6	4.5	65	2	P87455	P87455 lepidodacty
182	6	4.5	66	2	Q63AW0	Q63aw0 bacillus ce
183	6	4.5	67	2	Q73993	Q73993 pyrococcus
184	6	4.5	71	2	Q8VB36	Q8vb36 white spot
185	6	4.5	74	2	Q64Q17	Q64q17 bacteroides
186	6	4.5	76	1	RCRO_BPHKO	P18679 bacterioph
187	6	4.5	76	2	Q8WS66	Q8ws66 glossina mo
188	6	4.5	76	2	Q9PEQ8	Q9peq8 xylella fas
189	6	4.5	77	2	Q21983	Q21983 streptococc
190	6	4.5	80	2	Q74FL0	Q74fl0 geobacter s
191	6	4.5	81	2	Q24497	Q24497 drosophila
192	6	4.5	81	2	Q6MTN0	Q6mnt0 mycoplasma
193	6	4.5	82	2	Q6BQX0	Q6bqx0 debaryomyce
194	6	4.5	82	2	Q684N6	Q684n6 lactobacill
195	6	4.5	82	2	Q8D8S4	Q8d8e4 vibrio vuln
196	6	4.5	83	2	Q74003	Q74003 pyrococcus
197	6	4.5	83	2	Q6QXP5	Q6qxf5 agrotis seg
198	6	4.5	84	2	Q6CSM8	Q6csm8 yarrowia li
199	6	4.5	85	2	Q6G0I2	Q6g0i2 bartonella
200	6	4.5	86	1	SCRE_ARATH	P82633 arabidopsis
201	6	4.5	86	2	Q84IM3	Q84im3 clostridium
202	6	4.5	88	1	S61B_KLULA	Q8j2p4 kluyveromyc
203	6	4.5	88	2	Q6AM77	Q6am77 desulfotale
204	6	4.5	90	2	Q75BN7	Q75bn7 ashbya goss
205	6	4.5	90	2	Q6U6G1	Q6u6g1 human herpe
206	6	4.5	91	2	Q9BSG3	Q9bsg3 homo sapien
207	6	4.5	91	2	Q9YMG6	Q9ymg6 lymantria d
208	6	4.5	92	1	RR19_CHAGL	Q8m9us chaetosphae
209	6	4.5	92	1	RS19_THET2	P62660 thermus the
210	6	4.5	92	1	RS19_THETH	P80381 thermus the
211	6	4.5	92	2	Q7S7I9	Q7s7i9 neurospora
212	6	4.5	92	2	Q49587	Q49587 mycoplasma
213	6	4.5	93	2	Q9KL08	Q9kl08 vibrio chol
214	6	4.5	93	2	Q95334	Q95334 homo sapien
215	6	4.5	93	2	Q862Y0	Q862y0 bos taurus
216	6	4.5	97	2	Q6D0Z1	Q6d0z1 erwinia car
217	6	4.5	98	2	Q647N3	Q647n3 uncultured
218	6	4.5	98	2	Q63589	Q63589 florometra
219	6	4.5	99	2	Q6UB62	Q6ub62 hyaloperono
220	6	4.5	101	2	Q974Z5	Q974z5 sulfolobus
221	6	4.5	101	2	Q7N099	Q7n099 photorhabdu
222	6	4.5	101	2	Q81B80	Q81b80 bacillus ce
223	6	4.5	102	2	Q7R334	Q7r334 giardia lam
224	6	4.5	104	2	Q93V87	Q93v87 oryza sativ
225	6	4.5	106	2	Q9XVJ8	Q9xvj8 caenorhabdi
226	6	4.5	106	2	Q9KEL2	Q9kel2 bacillus ha
227	6	4.5	107	1	Y240_RICPR	Q9zdt5 rickettsia
228	6	4.5	107	1	Y324_RICCN	Q92iue rickettsia
229	6	4.5	107	2	Q7PB62	Q7pb62 rickettsia
230	6	4.5	107	2	Q68XC9	Q68xc9 rickettsia
231	6	4.5	108	2	Q8T329	Q8t329 plasmodium
232	6	4.5	108	2	Q8NQW8	Q8nqw8 corynebacte
233	6	4.5	109	2	Q7VCN9	Q7vcn9 prochloroco
234	6	4.5	110	1	RLA2_RHOGU	Q9vcu7 rhodotorula
235	6	4.5	110	2	Q8T5A7	Q8t5a7 plasmodium
236	6	4.5	110	2	Q6TST3	Q6tst3 bacillus sp
237	6	4.5	110	2	Q6TST5	Q6tst5 bacillus sp
238	6	4.5	110	2	Q6TST6	Q6tst6 bacillus sp
239	6	4.5	110	2	Q6TST7	Q6tst7 bacillus sp
240	6	4.5	110	2	Q6TST8	Q6tst8 bacillus sp
241	6	4.5	110	2	Q6TST9	Q6tst9 bacillus sp
242	6	4.5	110	2	Q6TSU0	Q6tsu0 bacillus sp
243	6	4.5	110	2	Q6TSU1	Q6tsu1 bacillus sp
244	6	4.5	110	2	Q6TSU3	Q6tsu3 bacillus sp
245	6	4.5	110	2	Q6TSU5	Q6tsu5 bacillus sp
246	6	4.5	110	2	Q6TSU8	Q6tsu8 bacillus sp
247	6	4.5	110	2	Q6TSV3	Q6tsv3 bacillus sp
248	6	4.5	110	2	Q6TSV4	Q6tsv4 bacillus sp
249	6	4.5	110	2	Q6TSW3	Q6tsw3 bacillus sp
250	6	4.5	110	2	Q6TSW5	Q6tsw5 bacillus sp

251	6	4.5	110	2	Q6TSW9	Q6tsw9 bacillus sp	324	6	4.5	146	2	Q6S8Z5	Q6s8z5 plasmodium
252	6	4.5	110	2	Q6TSX2	Q6tsx2 bacillus sp	325	6	4.5	146	2	Q6S8Z4	Q6s8z4 mycobacteri
253	6	4.5	110	2	Q6TSX3	Q6tsx3 bacillus sp	326	6	4.5	147	1	FUR_MYCTU	Q6s8z4 mycobacteri
254	6	4.5	110	2	Q6TSX4	Q6tsx4 bacillus sp	327	6	4.5	147	2	Q7REC7	Q7rfc7 plasmodium
255	6	4.5	110	2	Q6TSX7	Q6tsx7 bacillus sp	328	6	4.5	147	2	Q9LAL0	Q9lalo mycobacteri
256	6	4.5	110	2	Q6TSX8	Q6tsx8 bacillus sp	329	6	4.5	147	2	Q64ZR3	Q64zr3 bacteroides
257	6	4.5	110	2	Q6TSX9	Q6tsx9 bacillus sp	330	6	4.5	148	2	Q9EX95	Q9ex95 pseudomonas
258	6	4.5	110	2	Q6TSY7	Q6tsy7 bacillus ce	331	6	4.5	148	2	Q84143	Q84143 chlamydia t
259	6	4.5	110	2	Q6TSZ1	Q6tsz1 bacillus sp	332	6	4.5	148	2	Q7UEB1	Q7ueel rhodopirell
260	6	4.5	110	2	Q6TSZ2	Q6tsz2 bacillus sp	333	6	4.5	150	1	RL10_TOBAC	Q40592 nicotiana t
261	6	4.5	110	2	Q6TSZ3	Q6tsz3 bacillus sp	334	6	4.5	150	2	Q6V5E2	Q6v5e2 olimarabido
262	6	4.5	110	2	Q6DGM0	Q6dgm0 brachydanio	335	6	4.5	152	2	Q95XZ6	Q95x26 caenorhabdi
263	6	4.5	111	2	Q9FTX6	Q9ftx6 oryza sativ	336	6	4.5	152	2	Q8VLA1	Q8v141 streptococc
264	6	4.5	112	2	Q8W1C9	Q8w1c9 zea mays (m	337	6	4.5	152	2	Q8VVY6	Q8vvv6 streptococc
265	6	4.5	112	2	Q6K8U8	Q6k8u8 oryza sativ	338	6	4.5	152	2	Q8VVY7	Q8vvv7 streptococc
266	6	4.5	112	2	Q8ATF4	Q8atf4 castanea sa	339	6	4.5	152	2	Q8VVY8	Q8vvv8 streptococc
267	6	4.5	112	2	Q9ATW9	Q9atw9 zea mays (m	340	6	4.5	152	2	Q8VVY9	Q8vvv9 streptococc
268	6	4.5	112	2	Q98MI3	Q98mi3 rhizobium l	341	6	4.5	152	2	Q8VVZ0	Q8vvz0 streptococc
269	6	4.5	113	2	Q6B8P1	Q6b8p1 gracilaria	342	6	4.5	152	2	Q8XTH3	Q8xth3 raietonia s
270	6	4.5	114	1	S206_HUMAN	P80162 homo sapien	343	6	4.5	153	2	Q82RR6	Q82rr6 streptomyce
271	6	4.5	114	2	Q9RZG3	Q9rzg3 deinococcus	344	6	4.5	154	2	Q8SEW7	Q8sew7 cacopsylla
272	6	4.5	117	1	RNPA_THEMEA	Q9x1h4 thermotoga	345	6	4.5	156	1	AP19_YEAST	P35181 saccharomyc
273	6	4.5	118	2	Q64E23	Q64e23 uncultured	346	6	4.5	156	2	Q6FXK8	Q6fxk8 candida gla
274	6	4.5	118	2	Q9YAG7	Q9yag7 aeropyrum p	347	6	4.5	156	2	Q70ZG4	Q70z94 canis famil
275	6	4.5	118	2	Q8ZMQ6	Q8zmq6 salmonella	348	6	4.5	156	2	Q70ZG4	Q70z94 canis famil
276	6	4.5	119	2	Q93V10	Q93v10 arabidopsis	349	6	4.5	156	2	Q9M2T2	Q9m2t2 arabidopsis
277	6	4.5	120	2	Q58311	Q58311 pyrococcus	350	6	4.5	156	2	Q6S7M3	Q6s7m3 uncultured
278	6	4.5	120	2	Q77196	Q77196 plasmodium	351	6	4.5	156	2	Q8XLL8	Q8xll8 clostridium
279	6	4.5	121	1	ML30_ARATH	P33282 arabidopsis	352	6	4.5	157	1	VHCB_METVO	Q50849 methanococc
280	6	4.5	122	2	Q7SA46	Q7sa46 neurospora	353	6	4.5	157	2	Q8L8T8	Q8l8t8 arabidopsis
281	6	4.5	123	2	Q8ST88	Q8st88 plasmodium	354	6	4.5	157	2	Q9C8Y1	Q9c8y1 arabidopsis
282	6	4.5	124	2	Q8CTW6	Q8ctw6 staphylococ	355	6	4.5	157	2	Q7N3S4	Q7n3s4 photorhabdu
283	6	4.5	128	2	Q95W38	Q95w38 schistocerc	356	6	4.5	158	2	Q91C95	Q91c95 pan rhadino
284	6	4.5	128	2	Q6S8X6	Q6s8x6 plasmodium	357	6	4.5	159	2	Q74N72	Q74nj2 nanoarchaeu
285	6	4.5	128	2	Q9HXC8	Q9hxc8 pseudomonas	358	6	4.5	159	2	Q8RPA7	Q8rpa7 pseudomonas
286	6	4.5	129	1	Q98ML1	P34386 caenorhabdi	359	6	4.5	160	2	Q7XXS2	Q7xxs2 oryza sativ
287	6	4.5	131	2	Q98ML1	Q98ml1 rhizobium l	360	6	4.5	161	2	Q7PMF0	Q7pmf0 anopheles g
288	6	4.5	131	2	Q6MU42	Q6mu42 mycoplasma	361	6	4.5	162	2	Q7TFX4	Q7tfx4 rhesus cyto
289	6	4.5	131	2	Q7VNO4	Q7vno4 haemophilus	362	6	4.5	165	2	Q75SF2	Q75sf2 drosophila
290	6	4.5	131	2	Q99LW1	Q99lw1 mus musculu	363	6	4.5	165	2	Q7VM67	Q7vm67 haemophilus
291	6	4.5	132	2	Q6LZJ8	Q6lzt8 methanococc	364	6	4.5	166	1	VG17_BPPI2	P03686 bacteriophag
292	6	4.5	132	2	Q9BQX0	Q9bqx0 homo sapien	365	6	4.5	166	2	Q6CPI1	Q6cp11 kluveromyc
293	6	4.5	133	2	Q6ZS21	Q6zs21 homo sapien	366	6	4.5	166	2	Q6WCC1	Q6wcc1 serratia pr
294	6	4.5	133	2	Q8WS74	Q8wst4 perinereis	367	6	4.5	167	2	Q75SH2	Q75sh2 drosophila
295	6	4.5	133	2	Q9U511	Q9u511 manduca sex	368	6	4.5	167	2	Q64XB3	Q64xb3 bacteroides
296	6	4.5	133	2	Q9U513	Q9u513 manduca sex	369	6	4.5	167	2	Q8YX42	Q8yx42 anabaena sp
297	6	4.5	133	2	Q9FHG2	Q9fhg2 arabidopsis	370	6	4.5	167	2	Q98D81	Q98d81 rhizobium l
298	6	4.5	134	2	Q8T589	Q8t589 plasmodium	371	6	4.5	168	1	PLAS_POPNI	P00299 populus nig
299	6	4.5	134	2	Q92NY3	Q92ny3 rhizobium m	372	6	4.5	168	1	PLAT_POPNI	P11970 populus nig
300	6	4.5	135	2	Q6LY91	Q6ly91 methanococc	373	6	4.5	168	2	Q97WD3	Q97wd3 sulfolobus
301	6	4.5	135	2	Q9YBJ8	Q9ybj8 aeropyrum p	374	6	4.5	169	2	Q8UIT6	Q8uit6 pyrococcus
302	6	4.5	135	2	Q6S8X7	Q6s8x7 plasmodium	375	6	4.5	169	2	Q6XCE6	Q6xce6 carvus elap
303	6	4.5	135	2	Q8SFW6	Q8sfw6 cacopsylla	376	6	4.5	169	2	Q8RF59	Q8rf59 fusobacteri
304	6	4.5	137	2	Q8LHB2	Q8lhb2 oryza sativ	377	6	4.5	170	2	Q87J70	Q87j70 vibrio para
305	6	4.5	138	2	Q63BE4	Q63be4 bacillus ce	378	6	4.5	171	2	Q7UGP2	Q7ugp2 rhodopirell
306	6	4.5	138	2	Q738D3	Q738d3 bacillus ce	379	6	4.5	171	2	Q69504	Q69504 human herpe
307	6	4.5	138	2	Q6H1S8	Q6his8 bacillus th	380	6	4.5	172	2	Q9XLW7	Q9x1w7 leishmania
308	6	4.5	140	2	Q7Z477	Q7z477 homo sapien	381	6	4.5	172	2	Q6IUI31	Q6iui31 escherichia
309	6	4.5	140	2	Q824S1	Q824s1 chlamydophi	382	6	4.5	173	2	Q8WUC7	Q8wuc7 oryza sativ
310	6	4.5	140	2	Q8E124	Q8e124 shewanella	383	6	4.5	173	2	Q40650	Q40650 oryza sativ
311	6	4.5	140	2	Q9PJJ1	Q9pj1 chlamydia m	384	6	4.5	174	1	RECR_HABDU	Q30823 haemophilus
312	6	4.5	141	2	Q6S8P8	Q6s8p8 plasmodium	385	6	4.5	174	2	Q7S726	Q7s726 neurospora
313	6	4.5	141	2	Q84554	Q84554 chlamydia t	386	6	4.5	175	2	Q8TM14	Q8tm14 methanosarc
314	6	4.5	142	2	Q8ZT24	Q8zt24 pyrobaculum	387	6	4.5	176	2	Q8TF13	Q8tfl3 methanosarc
315	6	4.5	142	2	Q9Z7N3	Q9z7n3 chlamydia p	388	6	4.5	178	2	Q7V6S3	Q7v6s3 prochloroco
316	6	4.5	142	2	Q6D6B6	Q6d6b6 erwinia car	389	6	4.5	178	2	Q9DEQ7	Q9deq7 gallus gall
317	6	4.5	143	2	Q6S8Q0	Q6s8q0 plasmodium	390	6	4.5	180	1	RRF_CHLPN	Q9z7k6 chlamydia p
318	6	4.5	143	2	Q8DS73	Q8ds73 streptococc	391	6	4.5	180	2	Q8ESH2	Q8esh2 streptococc
319	6	4.5	144	2	Q8RYD4	Q8ryd4 ovis aries	392	6	4.5	181	2	Q8E543	Q8e543 streptococc
320	6	4.5	144	2	Q9Z2S8	Q9z2s8 rhizobium m	393	6	4.5	182	2	Q979F9	Q979f9 thermoplasm
321	6	4.5	144	2	Q8BF75	Q8bft5 m mus muscu	394	6	4.5	182	2	Q54202	Q54202 streptomyce
322	6	4.5	145	2	Q711H5	Q711h5 lactobacill	395	6	4.5	183	2	Q8DZS3	Q8dzs3 streptococc
323	6	4.5	146	2	Q6FNC9	Q6fnc9 candida gla	396	6	4.5	184	1	KAD2_ANASP	Q8z0m3 anabaena sp

397	6	4.5	184	2	Q96HR9	Q96hr9 homo sapien
398	6	4.5	184	2	Q96LMO	Q96lmo homo sapien
399	6	4.5	184	2	Q96GH7	Q96gh7 arabidopsis
400	6	4.5	185	2	Q8WFY6	Q8wfy6 lemis hirta
401	6	4.5	186	2	Q4SR9	Q4sr9 oryza sativ
402	6	4.5	186	2	Q68JS7	Q68js7 gopherus po
403	6	4.5	188	2	Q9AW09	Q9aw09 guillardia
404	6	4.5	188	2	Q8RDN2	Q8rdn2 fusobacteri
405	6	4.5	189	2	Q9SS03	Q9ss03 arabidopsis
406	6	4.5	189	2	Q92CL2	Q92cl2 listeria in
407	6	4.5	190	2	Q63RC3	Q63rc3 burkholderi
408	6	4.5	190	2	Q65NC7	Q65nc7 bacillus li
409	6	4.5	191	1	YK25_YEAST	YK25 yeast
410	6	4.5	191	2	Q264F8	Q264f8 schistoecic
411	6	4.5	191	2	Q6XHV6	Q6xhv6 drosophila
412	6	4.5	191	2	Q9K3Q0	Q9k3q0 streptomyce
413	6	4.5	192	1	KADA_METJJA	KADA_METJJA
414	6	4.5	193	2	Q9YEL3	Q9yel3 aeropyrum p
415	6	4.5	193	2	Q86LY0	Q86ly0 myxine glut
416	6	4.5	193	2	Q86LY1	Q86ly1 brachiosteo
417	6	4.5	193	2	Q81WB0	Q81wb0 bacillus an
418	6	4.5	195	2	Q97B70	Q97b70 thermoplas
419	6	4.5	198	2	Q69QA7	Q69qa7 oryza sativ
420	6	4.5	198	2	Q92XJ6	Q92xj6 rhizobium m
421	6	4.5	198	2	Q92N06	Q92n06 streptomyce
422	6	4.5	199	2	Q94WV1	Q94wv1 mastigoproce
423	6	4.5	201	1	Y802_NEIMA	Y802_NEIMA
424	6	4.5	201	2	Q8SQAS	Q8sqas neisseria m
425	6	4.5	201	2	Q8YNG8	Q8yng8 anabaena sp
426	6	4.5	202	1	COAT_ELV	COAT_ELV
427	6	4.5	202	1	Y598_NEIMB	Y598_NEIMB
428	6	4.5	202	2	Q93EK2	Q93ek2 saccharopol
429	6	4.5	202	2	Q9RG18	Q9rg18 bacteroides
430	6	4.5	202	2	Q9N3T9	Q9n3t9 photorhabdu
431	6	4.5	203	1	YL36_YEAST	YL36 yeast
432	6	4.5	204	2	Q8NIX6	Q8nix6 neosporea
433	6	4.5	204	2	Q8HJK8	Q8hjk8 brachidonte
434	6	4.5	204	2	Q8HJK9	Q8hjk9 brachidonte
435	6	4.5	204	2	Q8EMN1	Q8emn1 oceanobacil
436	6	4.5	205	2	Q61IL5	Q61il5 drosophila
437	6	4.5	205	2	Q34560	Q34560 geukensia d
438	6	4.5	205	2	Q66676	Q66676 equid herpe
439	6	4.5	207	2	Q9NX03	Q9nx03 homo sapien
440	6	4.5	207	2	Q7X1S5	Q7x1s5 pseudomonas
441	6	4.5	208	2	Q8A788	Q8a788 bacteroides
442	6	4.5	210	1	RL10_CHICK	RL10_CHICK
443	6	4.5	210	2	Q67A25	Q67a25 thalictum
444	6	4.5	210	2	Q62FC9	Q62fc9 burkholderi
445	6	4.5	210	2	Q83XL2	Q83xl2 burkholderi
446	6	4.5	210	2	Q87DE5	Q87de5 xyella fas
447	6	4.5	210	2	Q9PD54	Q9pd54 xyella fas
448	6	4.5	211	2	Q9CTD2	Q9ctd2 mus musculu
449	6	4.5	211	2	Q7RQK7	Q7rqk7 plasmodium
450	6	4.5	211	2	Q9QUL0	Q9qul0 rattus norv
451	6	4.5	211	2	Q9R0S7	Q9r0s7 rattus norv
452	6	4.5	212	1	RL10_PIG	RL10_PIG
453	6	4.5	212	2	Q7PFX12	Q7pfx12 anopheles g
454	6	4.5	212	2	Q8R7Q7	Q8r7q7 thermoanaer
455	6	4.5	213	1	RL10_BOVIN	RL10_BOVIN
456	6	4.5	213	1	RL10_HUMAN	RL10_HUMAN
457	6	4.5	213	1	RL10_MOUSE	RL10_MOUSE
458	6	4.5	213	1	RL10_RAT	RL10_RAT
459	6	4.5	213	2	Q8TDA5	Q8tda5 homo sapien
460	6	4.5	214	1	1432_SCHEMA	1432_SCHEMA
461	6	4.5	214	1	RL10_CABEL	RL10_CABEL
462	6	4.5	214	2	Q96L21	Q96l21 homo sapien
463	6	4.5	214	2	Q6LAG5	Q6lag5 suberites d
464	6	4.5	214	2	Q9FVN3	Q9fvn3 oryza sativ
465	6	4.5	214	2	Q97HN7	Q97hn7 clostridium
466	6	4.5	214	2	Q82315	Q82315 chlamydomo
467	6	4.5	214	2	Q87ZV3	Q87zv3 pseudomonas
468	6	4.5	214	2	Q89EB2	Q89eb2 bradyrhizob
469	6	4.5	214	2	Q89EB2	Q89eb2 bradyrhizob

Q66VF0	2	Q66VF0	2	214	4.5	6	470	Q96hr9 homo sapien
Q801H9	2	Q801H9	2	214	4.5	6	471	Q96lmo homo sapien
Q641S6	2	Q641S6	2	214	4.5	6	472	Q96gh7 arabidopsis
Q7PQZ6	2	Q7PQZ6	2	215	4.5	6	473	Q8wfy6 lemis hirta
Q6KIE5	2	Q6KIE5	2	215	4.5	6	474	Q4sr9 oryza sativ
Q88GV6	2	Q88GV6	2	215	4.5	6	475	Q68js7 gopherus po
Q6VTR3	2	Q6VTR3	2	215	4.5	6	476	Q9aw09 guillardia
Q90YV9	2	Q90YV9	2	215	4.5	6	477	Q8rdn2 fusobacteri
Q6DIQ8	2	Q6DIQ8	2	215	4.5	6	478	Q9ss03 arabidopsis
Q7ZVX6	2	Q7ZVX6	2	215	4.5	6	479	Q92cl2 listeria in
Q7ZXX4	2	Q7ZXX4	2	215	4.5	6	480	Q63rc3 burkholderi
SPR2_IPOBA	1	SPR2_IPOBA	1	216	4.5	6	481	Q65nc7 bacillus li
PI4716	2	PI4716	2	216	4.5	6	482	Q36138 saccharomyc
PI0965	2	PI0965	2	216	4.5	6	483	Q26468 schistoecic
Q970W9	2	Q970W9	2	216	4.5	6	484	Q6xhv6 drosophila
Q61C96	2	Q61C96	2	216	4.5	6	485	Q9k3q0 streptomyce
Q86G55	2	Q86G55	2	216	4.5	6	486	Q43409 methanococ
Q70Z95	2	Q70Z95	2	216	4.5	6	487	Q9yel3 aeropyrum p
Q40091	2	Q40091	2	216	4.5	6	488	Q86ly0 myxine glut
Q6DV42	2	Q6DV42	2	216	4.5	6	489	Q86ly1 brachiosteo
Q6DV76	2	Q6DV76	2	216	4.5	6	490	Q81wb0 bacillus an
Q7WAU4	2	Q7WAU4	2	216	4.5	6	491	Q97b70 thermoplas
Q8PV90	2	Q8PV90	2	217	4.5	6	492	Q69qa7 oryza sativ
Q83DJ4	2	Q83DJ4	2	217	4.5	6	493	Q92xj6 rhizobium m
RL10_ORYSA	1	RL10_ORYSA	1	218	4.5	6	494	Q92n06 streptomyce
Q61231	2	Q61231	2	218	4.5	6	495	Q94wv1 mastigoproce
Q6XIN5	2	Q6XIN5	2	218	4.5	6	496	Q9jvk3 neisseria m
Q96649	2	Q96649	2	219	4.5	6	497	Q8sqas bos taurus
Q96647	2	Q96647	2	219	4.5	6	498	Q8yng8 anabaena sp
RL10_BOMMA	1	RL10_BOMMA	1	219	4.5	6	499	Q35927 erysimum la
RL10_SOLME	2	RL10_SOLME	2	219	4.5	6	500	Q9k018 neisseria m
SPR1_IPOBA	1	SPR1_IPOBA	1	219	4.5	6	501	Q93ek2 saccharopol
SPRA_IPOBA	1	SPRA_IPOBA	1	219	4.5	6	502	Q9rg18 bacteroides
Q6UXZ8	2	Q6UXZ8	2	219	4.5	6	503	Q9n3t9 photorhabdu
Q9UXZ8	2	Q9UXZ8	2	219	4.5	6	504	Q8nix6 neosporea
Q95P53	2	Q95P53	2	219	4.5	6	505	Q8hjk8 brachidonte
Q95PD4	2	Q95PD4	2	219	4.5	6	506	Q8hjk9 brachidonte
Q6F451	2	Q6F451	2	219	4.5	6	507	Q8emn1 oceanobacil
Q6F451	2	Q6F451	2	219	4.5	6	508	Q61il5 drosophila
Q7PSW8	2	Q7PSW8	2	219	4.5	6	509	Q34560 geukensia d
Q8VWX0	2	Q8VWX0	2	219	4.5	6	510	Q66676 equid herpe
Q8VWX0	2	Q8VWX0	2	219	4.5	6	511	Q9nx03 homo sapien
Q40084	2	Q40084	2	219	4.5	6	512	Q7x1s5 pseudomonas
Q40085	2	Q40085	2	219	4.5	6	513	Q8a723 bacteroides
Q40085	2	Q40085	2	219	4.5	6	514	Q8a788 bacteroides
Q40092	2	Q40092	2	219	4.5	6	515	Q88200 gallus gall
Q9SWG8	2	Q9SWG8	2	219	4.5	6	516	Q67a25 thalictum
Q9ZSC7	2	Q9ZSC7	2	219	4.5	6	517	Q62fc9 burkholderi
Q7MAJ2	2	Q7MAJ2	2	219	4.5	6	518	Q83xl2 burkholderi
Q87ES3	2	Q87ES3	2	219	4.5	6	519	Q87de5 xyella fas
Q87es3	2	Q87es3	2	219	4.5	6	520	Q9pd54 xyella fas
Q9PGM0	2	Q9PGM0	2	219	4.5	6	521	Q9ctd2 mus musculu
Q810E5	2	Q810E5	2	219	4.5	6	522	Q7rqk7 plasmodium
RL10_EUPES	1	RL10_EUPES	1	220	4.5	6	523	Q9qul0 rattus norv
RL10_MAIZE	1	RL10_MAIZE	1	220	4.5	6	524	Q9r0s7 rattus norv
RL10_MAIZE	1	RL10_MAIZE	1	220	4.5	6	525	Q29195 sus scrofa
RL10_VITRI	2	RL10_VITRI	2	220	4.5	6	526	Q7pfx12 anopheles g
Q05942	2	Q05942	2	220	4.5	6	527	Q8R7Q7 thermoanaer
Q93VU9	2	Q93VU9	2	220	4.5	6	528	Q9xsl3 bos taurus
Q34213	2	Q34213	2	220	4.5	6	529	P27635 homo sapien
Q08770	2	Q08770	2	221	4.5	6	530	Q8zvw3 mus musculu
Q93W22	2	Q93W22	2	221	4.5	6	531	Q8pdv7 rattus norv
Q6MLU4	2	Q6MLU4	2	221	4.5	6	532	Q8tda5 homo sapien
Q8etg6	2	Q8etg6	2	221	4.5	6	533	Q26537 schistosoma
Q8etg6	2	Q8etg6	2	221	4.5	6	534	Q09533 caenorhabdi
Q8etg6	2	Q8etg6	2	221	4.5	6	535	Q96l21 homo sapien
Q8etg6	2	Q8etg6	2	221	4.5	6	536	Q6lag5 suberites d
Q8etg6	2	Q8etg6	2	221	4.5	6	537	Q9fvn3 oryza sativ
Q8etg6	2	Q8etg6	2	221	4.5	6	538	Q97hn7 clostridium
Q8etg6	2	Q8etg6	2	221	4.5	6	539	Q82315 chlamydomo
Q8etg6	2	Q8etg6	2	221	4.5	6	540	Q87zv3 pseudomonas
Q8etg6	2	Q8etg6	2	221	4.5	6	541	Q89eb2 bradyrhizob
Q8etg6	2	Q8etg6	2	221	4.5	6	542	Q89eb2 bradyrhizob

Q66VF0	2	Q66VF0	2	214	4.5	6	470	Q96hr9 homo sapien
Q801H9	2	Q801H9	2	214	4.5	6	471	Q96lmo homo sapien
Q641S6	2	Q641S6	2	214	4.5	6	472	Q96gh7 arabidopsis
Q7PQZ6	2	Q7PQZ6	2	215	4.5	6	473	Q8wfy6 lemis hirta
Q6KIE5	2	Q6KIE5	2	215	4.5	6	474	Q4sr9 oryza sativ
Q88GV6	2	Q88GV6	2	215	4.5	6	475	Q68js7 gopherus po
Q6VTR3	2	Q6VTR3	2	215	4.5	6	476	Q9aw09 guillardia
Q90YV9	2	Q90YV9	2	215	4.5	6	477	Q8rdn2 fusobacteri
Q6DIQ8	2	Q6DIQ8	2	215	4.5	6	478	Q9ss03 arabidopsis
Q7ZVX6	2	Q7ZVX6	2	215	4.5	6	479	Q92cl2 listeria in
Q7ZXX4	2	Q7ZXX4	2	215	4.5	6	480	Q63rc3 burkholderi
SPR2_IPOBA	1	SPR2_IPOBA	1	216	4.5	6	481	Q65nc7 bacillus li
PI4716	2	PI4716	2	216	4.5	6	482	Q36138 saccharomyc
PI0965	2	PI0965	2	216	4.5	6	483	Q26468 schistoecic
Q970W9	2	Q970W9	2	216	4.5	6	484	Q6xhv6 drosophila
Q61C96	2	Q61C96	2	216	4.5	6	485	Q9k3q0 streptomyce
Q86G55	2	Q86G55	2	216	4.5	6	486	Q43409 methanococ
Q70Z95	2	Q70Z95	2	216	4.5	6	487	Q9yel3 aeropyrum p

543	6	4.5	226	2	Q7WQW9	Q7wqw9 bordetella	616	6	4.5	249	2	Q6NZA9	Q6nza9 mus musculus
544	6	4.5	227	2	Q7VHS9	Q7vhs9 helicobacte	617	6	4.5	250	1	Y035_METJA	Q60350 methanococc
545	6	4.5	227	2	Q7VHS9	Q7vhs9 helicobacte	618	6	4.5	251	1	Y297_METJA	Q57745 methanococc
546	6	4.5	227	2	Q8G547	Q8g547 bifidobacte	619	6	4.5	251	2	Q9HBM6	Q9hbm6 homo sapien
547	6	4.5	227	2	Q9WH41	Q9wh41 human herpe	620	6	4.5	251	2	Q9Y283	Q9y283 homo sapien
548	6	4.5	228	1	EA5B_BRARE	P79728 brachydanio	621	6	4.5	251	2	Q6L199	Q6l199 drosophila
549	6	4.5	228	1	RL10_PINTA	Q22431 pinus taeda	622	6	4.5	251	2	Q7QF34	Q7qp34 giardia lam
550	6	4.5	228	1	Q6M0F2	Q6m0f2 methanococc	623	6	4.5	252	2	Q80WM6	Q80wm6 mus musculus
551	6	4.5	229	1	MODB_ECOLI	P09834 escherichia	624	6	4.5	253	1	TAF9_RAT	Q62880 rattus norv
552	6	4.5	229	1	Q8ZXF5	Q8zxr5 pyrobaculum	625	6	4.5	253	2	Q6CVM4	Q6cvm4 kluyveromyc
553	6	4.5	229	2	Q8XH21	Q8xh21 salmonella	626	6	4.5	254	2	Q8IXE7	Q8ixe7 homo sapien
554	6	4.5	229	2	Q7CQW7	Q7cq7 salmonella	627	6	4.5	254	2	Q27936	Q27936 fasciola he
555	6	4.5	229	2	Q87HN3	Q87hn3 vibrio para	628	6	4.5	254	2	Q98NV7	Q98nv7 rhizobium l
556	6	4.5	229	2	Q8FJR5	Q8fjr5 escherichia	629	6	4.5	254	2	Q83A76	Q83a76 coxiella bu
557	6	4.5	229	2	Q83SA6	Q83sa6 shigella fl	630	6	4.5	254	2	Q641A8	Q641a8 xenopus lae
558	6	4.5	229	2	Q9WHB1	Q9whb1 human herpe	631	6	4.5	255	2	Q8YX23	Q8yx23 anabaena sp
559	6	4.5	231	1	YE12_YEAST	P39975 saccharomyc	632	6	4.5	255	2	Q8CKN3	Q8ckn3 versinia pe
560	6	4.5	231	2	Q8B1N5	Q8bin5 saccharomyc	633	6	4.5	257	2	Q8GQA2	Q8gqa2 pseudomonas
561	6	4.5	231	2	Q8YLI5	Q8yli5 anabaena sp	634	6	4.5	258	2	Q98S77	Q98s77 guillardia
562	6	4.5	231	2	Q9CYI4	Q9cyi4 mus musculus	635	6	4.5	259	2	Q7PF71	Q7pf71 anopheles g
563	6	4.5	232	1	RNP3_METMP	P60781 methanococc	636	6	4.5	259	2	Q6UV34	Q6uv34 rattus norv
564	6	4.5	232	1	UBIG_PSEPK	Q88m10 pseudomonas	637	6	4.5	259	2	Q7TP20	Q7tp20 rattus norv
565	6	4.5	232	1	UBIG_PSESM	Q885t9 pseudomonas	638	6	4.5	260	2	Q7MU70	Q7mu70 porphyronon
566	6	4.5	232	2	Q2U7I6	Q2ute6 rhizobium m	639	6	4.5	261	1	COBS_RACHD	Q8kcn9 bacillus ha
567	6	4.5	232	2	Q97I18	Q97ie8 clostridium	640	6	4.5	261	2	Q66FP2	Q66fp2 versinia ps
568	6	4.5	233	1	BCLA_HUMAN	Q95999 h b cell ly	641	6	4.5	261	2	Q8ZAQ6	Q8zaq6 versinia pe
569	6	4.5	233	1	BCLA_RAT	Q95999 h b cell ly	642	6	4.5	261	2	Q9KGC6	Q9kgc6 bacillus ha
570	6	4.5	233	2	Q67NT0	Q67nt0 symbiobacte	643	6	4.5	262	2	Q6CTE9	Q6cte9 kluyveromyc
571	6	4.5	233	2	Q8G6E8	Q8g6e8 bifidobacte	644	6	4.5	262	2	Q9KHD9	Q9khd9 streptomyc
572	6	4.5	233	2	Q928V6	Q928v6 chlamydia p	645	6	4.5	262	2	Q8CJV4	Q8civ4 streptomyc
573	6	4.5	234	2	Q9H6D8	Q9h6d8 homo sapien	646	6	4.5	263	2	Q6XCF0	Q6xcf0 alces alces
574	6	4.5	234	2	Q935Q2	Q935q2 salmonella	647	6	4.5	264	1	TAF9_HUMAN	Q16594 homo sapien
575	6	4.5	235	2	Q8YT09	Q8yt09 anabaena sp	648	6	4.5	264	1	TAF9_MOUSE	Q8vi33 mus musculus
576	6	4.5	236	2	Q62HY4	Q62hy4 burkholderi	649	6	4.5	264	2	Q7PVAB	Q7pva8 anopheles g
577	6	4.5	238	2	Q221J5	Q221j5 arabidopsis	650	6	4.5	264	2	Q6XCE9	Q6xce9 ovis aries
578	6	4.5	238	2	Q53167	Q53167 rhizobium s	651	6	4.5	265	2	Q6L199	Q6l199 picrophilus
579	6	4.5	239	1	Y352_METJA	Q57798 methanococc	652	6	4.5	265	2	Q6FY89	Q6fy89 candida gla
580	6	4.5	239	2	Q8A704	Q8a704 bacteroides	653	6	4.5	266	2	Q72PQ3	Q72pq3 leptospira
581	6	4.5	239	2	Q8DMG3	Q8dmg3 synechococc	654	6	4.5	266	2	Q8F6K0	Q8f6k0 leptospira
582	6	4.5	240	2	Q73KH0	Q73kh0 treponema d	655	6	4.5	267	2	Q70K03	Q70k03 bacillus am
583	6	4.5	241	2	Q7PK32	Q7pk32 anopheles g	656	6	4.5	268	2	Q650W0	Q650w0 oryza sativ
584	6	4.5	241	2	Q7QLB6	Q7qlb6 anopheles g	657	6	4.5	268	2	Q98M34	Q98m34 rhizobium l
585	6	4.5	241	2	Q7A0U4	Q7a0u4 staphylococ	658	6	4.5	269	1	6PGL_CABEL	Q18229 caenorhabdi
586	6	4.5	241	2	Q7A2R6	Q7a2r6 staphylococ	659	6	4.5	269	2	Q9ZUA7	Q9zua7 arabidopsis
587	6	4.5	241	2	Q7A5H6	Q7a5h6 staphylococ	660	6	4.5	270	1	FLHO_BACSU	P39752 bacillus su
588	6	4.5	241	2	Q8CP56	Q8cp56 staphylococ	661	6	4.5	270	2	Q8L9Q4	Q8l9q4 arabidopsis
589	6	4.5	241	2	Q8DLI6	Q8dl16 synechococc	662	6	4.5	271	2	Q9SKU8	Q9skus arabidopsis
590	6	4.5	241	2	Q8DLT9	Q8dl19 synechococc	663	6	4.5	272	2	Q9F7L9	Q9ftl9 gamma-prote
591	6	4.5	241	2	Q9L524	Q9l524 staphylococ	664	6	4.5	273	2	Q7VTP1	Q7vtp1 bordetella
592	6	4.5	241	2	Q62076	Q62076 mus musculus	665	6	4.5	273	2	Q7W150	Q7w150 bordetella
593	6	4.5	242	2	Q7Q6I7	Q7q6i7 anopheles g	666	6	4.5	273	2	Q7WNU0	Q7wnu0 bordetella
594	6	4.5	242	2	Q7P642	Q7p642 fusobacteri	667	6	4.5	273	2	Q6D636	Q6d636 erwinia car
595	6	4.5	242	2	Q8RGQ1	Q8rgq1 fusobacteri	668	6	4.5	274	2	Q8VZ41	Q8vz41 arabidopsis
596	6	4.5	242	2	Q97N70	Q97n70 streptococc	669	6	4.5	275	2	Q88LI1	Q88li1 pseudomonas
597	6	4.5	242	2	Q8DMZ8	Q8dmz8 streptococc	670	6	4.5	276	2	Q9IC27	Q9ic27 human herpe
598	6	4.5	243	2	Q7NFY9	Q7nfy9 gloeobacter	671	6	4.5	277	2	Q6CIN5	Q6cin5 yarrowia li
599	6	4.5	243	2	Q8DMH9	Q8dm9 synechococc	672	6	4.5	278	1	URED_ECOLI	Q03285 escherichia
600	6	4.5	244	1	TPIS_DEIRA	Q8rups deinococcus	673	6	4.5	279	1	EFTS_BORBU	Q51148 borrelia bu
601	6	4.5	244	2	Q8FDL4	Q8fdl4 escherichia	674	6	4.5	279	1	Y144_MYCGE	P47390 mycoplasma
602	6	4.5	245	2	Q9VPM1	Q9vpm1 drosophila	675	6	4.5	279	2	Q93LC0	Q93lc0 salmonella
603	6	4.5	245	2	Q6YK36	Q6yk36 bacillus su	676	6	4.5	279	2	Q632P0	Q632p0 borrelia ga
604	6	4.5	245	2	Q97HU5	Q97hj5 clostridium	677	6	4.5	279	2	Q9CINN0	Q9cinn0 pasteurella
605	6	4.5	245	2	Q89FJ8	Q89fj8 bradyrhizob	678	6	4.5	279	2	Q99SA3	Q99sa3 human herpe
606	6	4.5	246	2	Q97YJ39	Q97y39 sulfolobus	679	6	4.5	279	2	Q995B6	Q995b6 human herpe
607	6	4.5	246	2	Q80W00	Q80w00 mus musculus	680	6	4.5	280	1	KD11_BACTN	Q8a284 bacteroides
608	6	4.5	247	2	Q970F9	Q970f9 sulfolobus	681	6	4.5	280	2	Q650K4	Q650k4 bacteroides
609	6	4.5	247	2	Q7QCB8	Q7qcb8 anopheles g	682	6	4.5	281	2	Q7WRR4	Q7wrr4 bartonella
610	6	4.5	247	2	Q6D1F6	Q6dlf6 erwinia car	683	6	4.5	281	2	Q7X255	Q7x255 bartonella
611	6	4.5	247	2	Q6G972	Q6g972 staphylococ	684	6	4.5	281	2	Q7X257	Q7x257 bartonella
612	6	4.5	247	2	Q6GGK6	Q6ggk6 staphylococ	685	6	4.5	281	2	Q7X261	Q7x261 bartonella
613	6	4.5	248	2	Q9VPM0	Q9vpm0 drosophila	686	6	4.5	282	2	Q7UGM3	Q7ugm3 rhodopirell
614	6	4.5	249	2	Q67X43	Q67x43 oryza sativ	687	6	4.5	283	2	Q64DP8	Q64dp8 uncultured
615	6	4.5	249	2	Q33598	Q33598 streptococc	688	6	4.5	283	2	Q67681	Q67681 aquifex aeo

689	6	4.5	283	2	Q83BH3	Q83bh3 coxiella bu	762	6	4.5	308	2	Q6CKS1	Q6cksl kluyveromyc
690	6	4.5	284	1	PURU_SYNV3	Q55135 synchocyst	763	6	4.5	308	2	Q7RNU9	Q7rnj9 plasmodium
691	6	4.5	284	2	Q8LBY7	Q8lby7 arabidopsis	764	6	4.5	308	2	Q8DYR9	Q8dyr9 streptococc
692	6	4.5	284	2	Q8LW57	Q8lw57 arabidopsis	765	6	4.5	308	2	Q68EQ7	Q68eq7 xenopus tro
693	6	4.5	284	2	O10617	O10617 helicoverpa	766	6	4.5	308	2	Q6GP78	Q6gp78 xenopus lae
694	6	4.5	284	2	Q91BY8	Q91by8 helicoverpa	767	6	4.5	308	2	Q7SZT8	Q7sztl xenopus lae
695	6	4.5	284	2	Q77L23	Q77l23 helicoverpa	768	6	4.5	308	2	Q7T390	Q7t390 brachydanio
696	6	4.5	284	2	Q801F0	Q801f0 xenopus lae	769	6	4.5	309	1	O4CD_HUMAN	Q8ngp0 homo sapien
697	6	4.5	285	2	Q6MX93	Q6mx93 azoarcus sp	770	6	4.5	309	1	PYRB_OCEIH	Q8er38 oceanobacil
698	6	4.5	286	2	O81013	O81013 arabidopsis	771	6	4.5	309	2	Q6XYV9	Q6xyv9 spioplasma
699	6	4.5	286	2	Q748Q2	Q748q2 geobacter s	772	6	4.5	310	2	Q97UW5	Q97uw5 sulfolobus
700	6	4.5	286	2	Q7NR69	Q7nr69 chromobacte	773	6	4.5	310	2	Q94961	Q94961 drosophila
701	6	4.5	289	2	Q9DSF1	Q9dsf1 human herpe	774	6	4.5	311	2	Q9CLL6	Q9cll6 pasteurella
702	6	4.5	290	1	Y2831_METUA	Q57731 methanococc	775	6	4.5	312	2	Q8NH20	Q8nh20 homo sapien
703	6	4.5	290	2	Q8L7C1	Q8l7c1 arabidopsis	776	6	4.5	312	2	Q94912	Q94912 drosophila
704	6	4.5	290	2	Q84WH6	Q84wh6 arabidopsis	777	6	4.5	312	2	Q9LK86	Q9lk86 arabidopsis
705	6	4.5	290	2	Q74CA5	Q74ca5 geobacter s	778	6	4.5	312	2	Q7TQV2	Q7tqv2 mus musculu
706	6	4.5	290	2	Q88C26	Q88c26 pseudomonas	779	6	4.5	313	1	SURA_HAEIN	R44721 haemophilus
707	6	4.5	290	2	Q9DSF2	Q9dsf2 human herpe	780	6	4.5	313	2	Q81FJ5	Q81fj5 drosophila
708	6	4.5	290	2	Q6F8A9	Q6f8a9 xenopus tro	781	6	4.5	313	2	Q9CAZ0	Q9caz0 arabidopsis
709	6	4.5	291	2	Q6ZBX9	Q6zbx9 oryza sativ	782	6	4.5	313	2	Q84FM7	Q84fm7 thermus aqu
710	6	4.5	291	2	Q9LX76	Q9lx76 arabidopsis	783	6	4.5	313	2	Q6MIP2	Q6mip2 bdellovibri
711	6	4.5	292	1	SDHA_PEPAS	P33073 peptostrept	784	6	4.5	314	2	Q7RSR0	Q7rsr0 plasmodium
712	6	4.5	293	2	Q7WVW5	Q7wvw5 streptococc	785	6	4.5	314	2	O6LGV3	O6lqv3 photobacter
713	6	4.5	293	2	Q745V5	Q745v5 thermus the	786	6	4.5	315	2	Q6FLH6	Q6flh6 candida gia
714	6	4.5	293	2	Q7TTH4	Q7ttw4 synchococc	787	6	4.5	315	2	Q9SCQ1	Q9scq1 arabidopsis
715	6	4.5	293	2	Q9CWN2	Q9cwn2 mus musculu	788	6	4.5	315	2	O5J9W1	Q5j9w1 neisseria m
716	6	4.5	293	2	Q6UED8	Q6ued8 xenopus lae	789	6	4.5	316	2	Q9M2H6	Q9m2h6 arabidopsis
717	6	4.5	294	1	VU51_HHVJ7	P52383 human herpe	790	6	4.5	317	2	Q96B32	Q96b32 homo sapien
718	6	4.5	294	2	Q834B2	Q834b2 enterococcu	791	6	4.5	317	2	O65KX5	O65kx5 bacillus li
719	6	4.5	294	2	Q77Y65	Q77y65 human herpe	792	6	4.5	318	2	O06629	O06629 mycobacteri
720	6	4.5	295	2	Q88QJ4	Q88qj4 lithobius f	793	6	4.5	318	2	O5J795	O5j795 mycobacteri
721	6	4.5	295	2	Q9SJD3	Q9sjd3 arabidopsis	794	6	4.5	318	2	Q7D9D6	Q7d9d6 mycobacteri
722	6	4.5	295	2	O83587	O83587 treponema p	795	6	4.5	318	2	Q7UI85	Q7ui85 mycobacteri
723	6	4.5	295	2	Q7MTI9	Q7mti9 porphyromon	796	6	4.5	319	1	YC39_PORPU	P51238 porphyra pu
724	6	4.5	296	2	Q7V103	Q7v103 prochloroco	797	6	4.5	319	2	O8VRJ3	O8vrj3 mus musculu
725	6	4.5	296	2	Q7W634	Q7w634 bordetella	798	6	4.5	319	2	Q9DGM0	Q9dgm0 gallus gall
726	6	4.5	296	2	Q7W100	Q7w100 bordetella	799	6	4.5	320	1	CY11_SOLTU	P25076 solanum tub
727	6	4.5	296	2	Q6KEK7	Q6keke7 xenopus lae	800	6	4.5	320	2	O855I5	O855i5 mycobacteri
728	6	4.5	297	1	FTR_METRA	P55301 methanosarc	801	6	4.5	320	2	Q41207	Q41207 solanum tub
729	6	4.5	297	2	Q7M819	Q7m819 wolinnella s	802	6	4.5	320	2	O8XI86	O8xi86 clostridium
730	6	4.5	298	1	OCRC_AGRU	Q00679 agrobacteri	803	6	4.5	320	2	O8XVQ6	O8xvq6 ralstonia s
731	6	4.5	298	2	Q9SLX1	Q9slx1 arabidopsis	804	6	4.5	321	1	TRYC_HUMAN	Q9nr12 homo sapien
732	6	4.5	299	2	Q37U89	Q37u89 sulfolobus	805	6	4.5	321	2	Q96RZ8	Q96rz8 homo sapien
733	6	4.5	299	2	Q89YF2	Q89yf2 bacteroides	806	6	4.5	321	2	Q67NQ4	Q67mq4 symbiobacte
734	6	4.5	300	2	Q6SKU9	Q6sku9 bacillus li	807	6	4.5	321	2	Q6NEJ5	Q6nbj5 rhodopseudo
735	6	4.5	300	2	O34990	O34990 bacillus su	808	6	4.5	321	2	Q7NGV0	Q7ngv0 photorhabdu
736	6	4.5	300	2	Q88E64	Q88e64 pseudomonas	809	6	4.5	322	2	O8NSY8	O8nsy8 homo sapien
737	6	4.5	300	2	Q9HXB6	Q9hxb6 pseudomonas	810	6	4.5	322	2	Q8UJU0	Q8uju0 agrobacteri
738	6	4.5	301	1	Y186_MYCPN	P75265 mycoplasma	811	6	4.5	322	2	O8YY66	O8yy66 anabaena sp
739	6	4.5	301	2	Q8WEY3	Q8wey3 septifer vi	812	6	4.5	322	2	O8GZV1	Q8gzv1 bruceella su
740	6	4.5	301	2	Q67Z40	Q67z40 arabidopsis	813	6	4.5	322	2	Q8CC71	Q8cc71 mus musculu
741	6	4.5	301	2	Q82F88	Q82f88 streptomyc	814	6	4.5	322	2	Q7TMM8	Q7tm88 mus musculu
742	6	4.5	301	2	O91BU8	O91bu8 helicoverpa	815	6	4.5	323	2	O6PK64	O6pk64 homo sapien
743	6	4.5	301	2	Q77LW4	Q77lw4 helicoverpa	816	6	4.5	324	2	Q758I8	Q758i8 ashbya goss
744	6	4.5	301	2	Q9E225	Q9e225 helicoverpa	817	6	4.5	324	2	Q9UXL0	Q9uxl0 neisseria m
745	6	4.5	302	2	Q9C4R6	Q9c4r6 methanosarc	818	6	4.5	325	2	Q95W95	Q95w95 crithidia f
746	6	4.5	302	2	Q6BQK3	Q6bqk3 debaryomyce	819	6	4.5	325	2	O630A6	O630a6 bacillus li
747	6	4.5	302	2	Q7TU88	Q7tuv8 prochloroco	820	6	4.5	325	2	O65PL5	O65pl5 bacillus li
748	6	4.5	303	2	P87589	P87589 citrus tris	821	6	4.5	325	2	Q7VCH0	Q7vch0 prochloroco
749	6	4.5	304	2	O942X6	O942x6 oryza sativ	822	6	4.5	326	1	DED2_HUMAN	O8wx18 homo sapien
750	6	4.5	304	2	O66991	O66991 aquifex aeo	823	6	4.5	326	2	Q9KWR0	Q9kwr0 bacillus sp
751	6	4.5	304	2	Q7UY63	Q7uy63 rhodospirell	824	6	4.5	327	2	Q7NNM39	Q7nm39 gloeobacter
752	6	4.5	305	2	Q7Q874	Q7q874 anopheles g	825	6	4.5	327	2	Q89NF9	Q89nf9 bradyrhizob
753	6	4.5	305	2	O67885	O67885 aquifex aeo	826	6	4.5	327	2	Q8D2M7	Q8d2m7 wigglewort
754	6	4.5	306	2	O86SN0	O86sn0 homo sapien	827	6	4.5	327	2	Q8N131	Q8n131 human herpe
755	6	4.5	307	1	YL72_ARCFU	Q28110 archaeoglob	828	6	4.5	327	2	Q7ZTA1	Q7zta1 brachydanio
756	6	4.5	307	2	Q4962	Q4962 drosophila	829	6	4.5	329	2	Q8U8N0	Q8u8n0 agrobacteri
757	6	4.5	307	2	Q8NT50	Q8nte0 corynebacte	830	6	4.5	330	1	DED2_MOUSE	Q8qzv0 mus musculu
758	6	4.5	307	2	G6PC24	G6pc24 brachydanio	831	6	4.5	330	2	Q6EGR7	Q6egr7 gonatocerus
759	6	4.5	308	1	GSN2_HUMAN	Q9nz01 homo sapien	832	6	4.5	330	2	Q858T2	Q858t2 bacterioph
760	6	4.5	308	1	GSN2_MOUSE	Q9cy27 mus musculu	833	6	4.5	330	2	Q7V2N4	Q7v2n4 prochloroco
761	6	4.5	308	1	GSN2_RAT	Q64232 rattus norv	834	6	4.5	331	2	Q6NB10	Q6nb10 rhodopseudo

835	6	4.5	331	2	Q7VDX4	Q7vdx4 prochloroco	908	2	Q6PIA3	Q6pia3 homo sapien
836	6	4.5	331	2	Q6IRJ6	Q6irj6 rattus norv	909	2	Q8I2L3	Q8i2l3 plasmodium
837	6	4.5	331	2	Q3JL55	Q3jl55 rattus norv	910	2	Q8PJC3	Q8pjc3 xanthomonas
838	6	4.5	332	2	Q759U4	Q759u4 aebhya goss	911	2	Q8XNA0	Q8xna0 clostridium
839	6	4.5	332	2	Q71S47	Q71s47 ophiopholis	912	2	Q6C0J3	Q6c0j3 yarrowia li
840	6	4.5	332	2	Q97QC7	Q97qc7 streptococc	913	2	Q966A1	Q966a1 caenorhabdi
841	6	4.5	332	2	Q7V372	Q7v372 prochloroco	914	2	Q6H742	Q6h742 oryza sativ
842	6	4.5	333	2	Q8PM92	Q8pm92 xanthomonas	915	2	Q6JZA7	Q6jza7 escherichia
843	6	4.5	333	2	Q87PK6	Q87fk6 vibrio para	916	2	Q6JZB1	Q6jzb1 escherichia
844	6	4.5	334	1	ALG5_YEAST	P40350 saccharomyc	917	2	Q9NG28	Q9ng28 planotortri
845	6	4.5	334	1	Y472_RICPR	Q9zd72 rickettsia	918	2	Q87J69	Q87j69 vibrio para
846	6	4.5	334	2	O14125	O14125 schizosacch	919	2	Q8V5T6	Q8v5t6 helicoverpa
847	6	4.5	334	2	Q6VPL9	Q6vpl9 salmonella	920	2	FUS3_YEAST	P16892 saccharomyc
848	6	4.5	334	2	Q6F1R6	Q6f1r6 mesoplasma	921	2	Q94G17	Q94g17 pisum sativ
849	6	4.5	335	2	Q8TML1	Q8tml1 methanosarc	922	2	Q6JZA8	Q6jza8 escherichia
850	6	4.5	335	2	Q3PLP4	Q3plp4 chlamydia m	923	2	Q6JZB4	Q6jzb4 escherichia
851	6	4.5	336	2	Q6ZNF1	Q6znf1 homo sapien	924	2	Q6JZC0	Q6jzc0 escherichia
852	6	4.5	336	2	Q8GNA9	Q8gna9 streptomyc	925	2	Q6JZD3	Q6jzd3 escherichia
853	6	4.5	336	2	Q9F8T0	Q9f8t0 streptomyc	926	2	Q6JZD4	Q6jzd4 escherichia
854	6	4.5	336	2	Q72R03	Q72r03 leptospira	927	2	Q63I88	Q63i88 burkholderi
855	6	4.5	336	2	Q8F4T4	Q8f4t4 leptospira	928	2	Q65UX4	Q65ux4 manheimia
856	6	4.5	337	2	Q6ZQV3	Q6zqv3 homo sapien	929	2	RFL_THETH	P96077 thermus the
857	6	4.5	337	2	Q9N382	Q9n382 caenorhabdi	930	2	Q6JZD1	Q6jzd1 escherichia
858	6	4.5	337	2	Q7CTZ4	Q7ctz4 agrobacteri	931	2	Q6JZD2	Q6jzd2 escherichia
859	6	4.5	337	2	Q8CQU8	Q8cqu8 oceanobacil	932	2	Q72HB8	Q72hb8 thermus the
860	6	4.5	337	2	Q8DHQ2	Q8dhq2 synechococc	933	2	Q8e4f3	Q8e4f3 streptococc
861	6	4.5	337	2	Q8E211	Q8e211 carcopithec	934	2	Q8e4f5	Q8e4f5 streptococc
862	6	4.5	338	2	Q6C582	Q6c582 yarrowia li	935	2	Q8e4f5	Q8e4f5 streptococc
863	6	4.5	338	2	Q8LB09	Q8lb09 arabidopsis	936	2	Q8e4f5	Q8e4f5 streptococc
864	6	4.5	338	2	Q9C9D0	Q9c9d0 arabidopsis	937	2	Q8e4f5	Q8e4f5 streptococc
865	6	4.5	338	2	Q8XQ11	Q8xq11 ralsctonia s	938	2	Q8HDV5	Q8hdv5 carabus vig
866	6	4.5	338	2	Q9K5W3	Q9k5w3 bacillus ha	939	2	Q8HDV6	Q8hdv6 carabus vig
867	6	4.5	339	1	TRAI_COXBU	Q45968 coxiella bu	940	2	Q8HDV7	Q8hdv7 carabus vig
868	6	4.5	339	2	Q87Y21	Q87y21 sulfolobus	941	2	Q8HDV9	Q8hdv9 carabus lat
869	6	4.5	339	2	Q8FQC4	Q8fqc4 candida gia	942	2	Q8HDW0	Q8hdw0 carabus pee
870	6	4.5	339	2	Q9Z199	Q9z199 lactobacill	943	2	Q8HDW3	Q8hdw3 carabus koi
871	6	4.5	339	2	Q8CX99	Q8cx99 oceanobacil	944	2	Q8HDW4	Q8hdw4 carabus par
872	6	4.5	339	2	Q70411	Q70411 rattus norv	945	2	Q8HDW5	Q8hdw5 carabus don
873	6	4.5	340	2	Q9XMP1	Q9xmp1 ceratitidis c	946	2	Q8HDW6	Q8hdw6 carabus obl
874	6	4.5	340	2	Q8YCH1	Q8ych1 mus musculu	947	2	Q8HDW7	Q8hdw7 carabus yun
875	6	4.5	340	2	Q7ZV12	Q7zv12 brachydanio	948	2	Q8HDW8	Q8hdw8 carabus mor
876	6	4.5	341	2	Q8THW7	Q8thw7 methanosarc	949	2	Q8HDW9	Q8hdw9 carabus nes
877	6	4.5	341	2	Q9NB46	Q9nb46 caenorhabdi	950	2	Q8HDX0	Q8hdx0 carabus nan
878	6	4.5	341	2	Q95B78	Q95b78 gymnotalaena	951	2	Q6JZA6	Q6jza6 escherichia
879	6	4.5	341	2	Q95B84	Q95b84 gymnotalaena	952	2	Q6JZA6	Q6jza6 escherichia
880	6	4.5	341	2	Q95B85	Q95ba5 dysnodia pi	953	2	Q6JZA6	Q6jza6 escherichia
881	6	4.5	341	2	Q95B85	Q95bb2 dysnodia pa	954	2	Q6JZD0	Q6jzd0 schizosacch
882	6	4.5	341	2	Q95B84	Q95bb4 boeberoides	955	2	Q84QU2	Q84qu2 oryza sativ
883	6	4.5	341	2	Q95B84	Q95bb4 boeberoides	956	2	Q93IP4	Q93ip4 synechococc
884	6	4.5	341	2	Q8K2P7	Q8k2f7 oryza sativ	957	2	Q6JZB8	Q6jzb8 escherichia
885	6	4.5	341	2	Q8YEZ0	Q8yez0 brucella me	958	2	Q7RDD9	Q7rdd9 plasmodium
886	6	4.5	341	2	Q8ES16	Q8es16 oceanobacil	959	2	Q7PDY8	Q7pdy8 fusobacteri
887	6	4.5	341	2	Q80ZU1	Q80zul mus musculu	960	2	Q7TDD5	Q7tdd5 tomato leaf
888	6	4.5	341	2	Q6GMG4	Q6gm94 brachydanio	961	2	Q7TDD5	Q7tdd5 tomato leaf
889	6	4.5	342	1	AN1H_HUMAN	P61962 homo sapien	962	2	Q9AVE6	Q9ave6 oryza sativ
890	6	4.5	342	1	AN1H_MOUSE	P61963 mus musculu	963	2	Q9AVE6	Q9ave6 oryza sativ
891	6	4.5	342	2	Q7R4G3	Q7r4g3 giardia lam	964	2	Q9AVE6	Q9ave6 oryza sativ
892	6	4.5	342	2	Q65Q84	Q65q84 manheimia	965	2	Q9ZL1	Q9ztl1 sulfolobus
893	6	4.5	342	2	Q8F648	Q8f648 xenopus tro	966	2	Q96CC2	Q96cc2 homo sapien
894	6	4.5	342	2	Q7ZY00	Q7zy00 xenopus lae	967	2	Q6JZA9	Q6jza9 escherichia
895	6	4.5	343	2	Q95B94	Q95b94 schizotrich	968	2	Q9F3K1	Q9f3k1 streptomyc
896	6	4.5	343	2	Q7ZY86	Q7zy86 xenopus lae	969	2	Q9C899	Q9c899 arabidopsis
897	6	4.5	344	2	Q8WY52	Q8wy52 homo sapien	970	2	Q9LHN8	Q9lhn8 arabidopsis
898	6	4.5	344	2	Q73MW5	Q73mw5 treponema d	971	2	Q7MAW9	Q7maw9 porphyronon
899	6	4.5	345	2	Q86403	Q8e403 methanobact	972	2	Q7UGV3	Q7ugv3 rhodospirill
900	6	4.5	345	2	Q8XL96	Q8xl96 clostridium	973	2	Q8FBR9	Q8fbr9 escherichia
901	6	4.5	346	2	Q65M77	Q65m77 bacillus li	974	2	Q8JZ15	Q8jz15 tomato leaf
902	6	4.5	347	2	Q697K7	Q697k7 aulacoseira	975	2	Q80A85	Q80a85 tomato leaf
903	6	4.5	347	2	Q6JZA5	Q6jza5 escherichia	976	2	Q80A85	Q80a85 tomato leaf
904	6	4.5	348	1	MER_METKA	Q8txy4 methanopyru	977	2	Q820W2	Q820w2 coxiella bu
905	6	4.5	348	2	Q9TD13	Q9tdl3 maratecoara	978	2	Q67NT4	Q67nt4 arabidopsis
906	6	4.5	349	2	Q704B5	Q704b5 thermoprote	979	2	Q9F720	Q9f720 chlorobium
907	6	4.5	349	2	Q6CUD6	Q6cuu6 kluyveromyc	980	2	Q6P207	Q6p207 mus musculu

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981 ID Q80VB6 mus musculus
982 AC Q8VDT3 mus musculus
983 P48535 kluyveromyc
984 Q966A0 caenorhabdi
985 Q91B45 pan rhadino
986 Q20005 caenorhabdi
987 Q06850 synechococc
988 Q6JZA3 escherichia
989 Q6JZD7 escherichia
990 Q6JZD7 escherichia
991 Q7JLJ3 caenorhabdi
992 Q8RBY5 thermoanaer
993 P44509 haemophilus
994 Q6BSI6 debaryomyce
995 QXEF7 oryza sativ
996 Q6LKC1 ureaplasma
997 Q9PPP4 ureaplasma
998 Q7XEC2 oryza sativ
999 Q6JZC9 escherichia
1000 Q6JZ88 escherichia

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ALIGNMENTS

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RESULT 1
ID Q76LV9 PRELIMINARY; PRT; 373 AA.
AC Q76LV9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Spop (fragment).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (SFP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB071989; BAB68542.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR SMART; SM00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS50144; MATH; 1.
FT NON TER 1
SQ SEQUENCE 373 AA; 42001 MW; BB4D75653FF0E47A CRC64;

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Query Match 100.0%; Score 132; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 9.6e-131;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMTINNFSCREMGVVKSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 60
Db 32 SYMTINNFSCREMGVVKSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 91
Qy 61 CPKSEVRAKFSILNAKGETKAMESQRAYRFVQKDWGPKFKFIRRDLLDEANGLLPD 120
Db 92 CPKSEVRAKFSILNAKGETKAMESQRAYRFVQKDWGPKFKFIRRDLLDEANGLLPD 151
Qy 121 DKLTLFCEVSVV 132
Db 152 DKLTLFCEVSVV 163

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RESULT 2
SPOP_HUMAN STANDARD; PRT; 374 AA.
ID SPOP_HUMAN
AC O43791;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Speckle-type POZ protein.
GN Name=SPOP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=98074898; PubMed=9414087; DOI=10.1016/S0014-5793(97)01340-9;
RA Nagai Y., Kojima T., Muro Y., Hachiya T., Nishizawa Y.,
RA Wakabayashi T., Hagiwara M.;
RT "Identification of a novel nuclear speckle-type protein, SPOP.";
RL FEBS Lett. 418:23-26(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix, and Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.J., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Inhibits IPFI/PDX1 transactivation of established target
CC promoters, such as insulin, may be by recruiting a repressor
CC complex (By similarity).
CC -!- SUBUNIT: Interacts with IPFI/PDX1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- MISCELLANEOUS: Antigen recognized by serum from scleroderma
CC patient.
CC -!- SIMILARITY: Contains 1 BTB/POZ domain.
CC -!- SIMILARITY: Contains 1 MATH domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ000644; CAA04199.1; -.
DR EMBL; BC001269; AAH01269.1; -.
DR EMBL; BC003385; AAH03385.1; -.
DR Genew; HGNC:11254; SPOP.
DR H-InvDB; HIX0013962; -.
DR MIM; 602850; -.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0006397; P:mRNA processing; TAS.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR002083; MATH.

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC75799.
GN Name=MGC75799;
OS Xenopus tropicalis (western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez Y., Bouffard G.G.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhards D.S.;
RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC061316; AAH61316.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR00210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS50144; MATH; 1.
KW Hypothetical protein.
SQ SEQUENCE 374 AA; 42154 MW; 2DC5738E57025BF7 CRC64;

Query Match 100.0%; Score 132; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 9.6e-131;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLCLRVNPKGLDEESKDYLSLYLLVS 60
Db 33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLCLRVNPKGLDEESKDYLSLYLLVS 92

Qy 61 CPKSEVRAPKFSILNAKGEETKAMESQRAYRFVQKDWGFKFKFIRRDFLDDEANGLLPD 120
Db 93 CPKSEVRAPKFSILNAKGEETKAMESQRAYRFVQKDWGFKFKFIRRDFLDDEANGLLPD 152

Qy 121 DKLTLFCEVSVV 132
Db 153 DKLTLFCEVSVV 164

RESULT 5
Q7T330 PRELIMINARY; PRT; 374 AA.
ID Q7T330
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Q7ZX06 PRELIMINARY; PRT; 374 AA.
Q7ZX06; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C9924-prov protein.
GN Name=c9924-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN RFL
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins C.M., Wagner L., Shenmen G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC046272; AHA46272.1; -
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS01044; MATH; 1.
SQ SEQUENCE 374 AA; 42154 MW; 2DC5738E57025BF7 CRC64;
Query Match 100.0%; Score 132; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 9.6e-131; Mismatches 0; Gaps 0;
Matches 132; Conserved 0; Indels 0;
QY 1 SYMMTINNFSFCREEMGEVKSSTPSSGANDKLMCLRVNPKGLDEESKDYLSLYLLVS 60
DB 33 SYMMTINNFSFCREEMGEVKSSTPSSGANDKLMCLRVNPKGLDEESKDYLSLYLLVS 92
QY 61 CPKSEVRKFKPSILNAKEETKAMESQRAVRFVQKDWGPKFKFTRRDFLDEANGLLPD 120
DB 93 CPKSEVRKFKPSILNAKEETKAMESQRAVRFVQKDWGPKFKFTRRDFLDEANGLLPD 152

QY 121 DKLTFLFCEVSVV 132
DB 153 DKLTFLFCEVSVV 164
RESULT 7
Q9DBZ2 PRELIMINARY; PRT; 425 AA.
Q9DBZ2; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE clone:120009E17 product:speckle-type POZ protein, full insert
DE sequence.
GN Name=Spop;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-3;
RA Carninci P., Hayashizaki Y.;
RL "High-efficiency full-length cDNA cloning";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RL "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX The FANTOM Consortium;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipette sequencer";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX Adachi J., Aizawa K., Akabira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

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RA Mateuyama T., Miyazaki A., Nishi K., Nomura K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saico H., Saico R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK04669; BAB23458.1; -.
DR MGD; MG1:1343085; Spop.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR00210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS00144; MATH; 1.
DR PROSITE; PS0144; MATH; 1.
SQ SEQUENCE 425 AA; 47514 MW; 7B6716666C3D884B CRC64;

Query Match 100.0%; Score 132; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.1e-130;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMTINNFSRCREMGVIVKSTFSSGANDKLKWLKLVNPKGLDERSKDYLSYLLVLS 60
Db 33 SYMTINNFSRCREMGVIVKSTFSSGANDKLKWLKLVNPKGLDERSKDYLSYLLVLS 92
Qy 61 CPKSEVRKPKFSILNAKGETKAMESORAYRVQGDWGFKKFIRDRFLDDEANGLLPD 120
Db 93 CPKSEVRKPKFSILNAKGETKAMESORAYRVQGDWGFKKFIRDRFLDDEANGLLPD 152
Qy 121 DKLTLCFCEVSVV 132
Db 153 DKLTLCFCEVSVV 164

RESULT 8
Q9HAB2 ID Q9HAB2 PRELIMINARY; PRT; 391 AA.
AC Q9HAB2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ11857.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura T., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto K., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kinata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Mueshino K., Yatsu H., Ohshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
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RA Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Itagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK021919; BAB13937.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR00210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS0144; MATH; 1.
DR PROSITE; PS0144; MATH; 1.
SQ SEQUENCE 391 AA; 44874 MW; 90DC2449E9141FD7 CRC64;

Query Match 40.2%; Score 53; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.7e-47;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESORAYRVQGDWGFKKFIRDRFLDDEANGLLPDKLTLCFCEVSVV 132
Db 112 EETKAMESORAYRVQGDWGFKKFIRDRFLDDEANGLLPDKLTLCFCEVSVV 164

RESULT 9
Q6IQ16 ID Q6IQ16 PRELIMINARY; PRT; 392 AA.
AC Q6IQ16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein LOC339745.
GN Name=LOC339745;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton D., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
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RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071613; AAH71613.1; -
DR GO; GO:0005515; P:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM0061; BTB; 1.
DR SMART; SM0061; MATH; 1.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS50144; MATH; 1.
KW Hypothetical protein.
SQ SEQUENCE 392 AA; 44647 MW; CEB4243BD732DFEF CRC64;

Query Match 40.2%; Score 53; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.7e-47;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 80 EETXAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPDDKLTFLFCEVSW 132
Db 112 EETXAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPDDKLTFLFCEVSW 164
|||||

RESULT 10
Q8MRB4 PRELIMINARY; PRT; 374 AA.
AC Q8MRB4; Q9VFP3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE R334508P (CG9924-PB).
GN ORFNames=CG9924;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhou Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY121682; AAM52009.1; -
DR EMBL; AE003702; AAN14348.1; -
DR IntAct; Q8MRB4; -
DR FlyBase; Fgn0038192; CG9924.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50097; BTB; 1.

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DR PROSITE: PS50144; MATH; 1.
SQ SEQUENCE 374 AA; 42283 MW; 2116548EB64F04C0 CRC64;

Query Match 30.3%; Score 40; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQKDWGFKFKFIRDFLLDEANGLLP 119
Db 112 BETKAMESQRAYRFVQKDWGFKFKFIRDFLLDEANGLLP 151

RESULT 11
Q7PGC0 PRELIMINARY; PRT; 401 AA.
AC Q7PGC0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE ENSANGP0000024127 (Fragment).
GN Name=ENSANGG0000011135;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA0801008851; EAA44989.1; -.
GO GO:0005515; F:protein binding; IEA.
DR InterPro; IPR002010; BTB POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS50144; MATH; 1.
FT NON TER 1
SQ SEQUENCE 401 AA; 45025 MW; 7769BD4FC20DFB86 CRC64;

Query Match 30.3%; Score 40; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.2e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQKDWGFKFKFIRDFLLDEANGLLP 119
Db 139 BETKAMESQRAYRFVQKDWGFKFKFIRDFLLDEANGLLP 178

RESULT 12
Q8ING4 PRELIMINARY; PRT; 403 AA.
AC Q8ING4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG924-PC (CG924-pd) (RE74593p).
GN ORFNames=CG9924;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt C., Nelson C.R., Gabor G.L.,
RA Brill J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balaw R.M., Baau A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennish J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RN melanogaster euchromatic genome sequence.";
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RN a genomics perspective.";
RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RN systematic review.";
RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;

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RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003702; AAN14346.1; -
DR EMBL; BT012443; AAS93714.1; -
DR FLYBASE; FBgn0038192; CG9924.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTF_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTF; 1.
DR SMART; SM00225; BTF; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50097; BTF; 1.
DR PROSITE; PS50144; MATH; 1.
SQ SEQUENCE 403 AA; 45310 MW; 190BBS5EC3B108CD8 CRC64;

Query Match 30.3%; Score 40; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 2.2e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQGWGFKFIRDRDLDLDEANGLLP 119
Db 141 EETKAMESQRAYRFVQGWGFKFIRDRDLDLDEANGLLP 180

RESULT 13
Q7KSK6
ID Q7KSK6 PRELIMINARY; PRT; 406 AA.
AC Q7KSK6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
GN CG9924-PA.
DB ORFNames=CG9924;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.R., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Massarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Beriman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003702; AAF55007.3; -
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTF_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTF; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTF; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50097; BTF; 1.
DR PROSITE; PS50144; MATH; 1.
SQ SEQUENCE 406 AA; 45750 MW; 344A5EA7A271D404 CRC64;

Query Match 30.3%; Score 40; DB 2; Length 406;

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Best Local Similarity 100.0%; Pred. No. 2.2e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLP 119
|||||
Db 144 EETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLP 183
|||||

RESULT 14

ID YNV5 CAEEL STANDARD; PRT; 451 AA.
AC P34568;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein T16H12.5 in chromosome III.
GN ORFNames=T16H12.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018(1998).
RN [2]

RP REVISIONS.

RA Durbin R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BTB/POZ domain.
CC -1- SIMILARITY: Contains 1 MATH domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
CC -----

DR EMBL; Z30662; CAAB3138.2; -
DR WormBase; WBGene00011815; T16H12.5.
DR WormPep; T16H12.5; CE29054.
DR InterPro; IPR000210; BTB POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS0144; MATH; 1.
KW Hypothetical protein.
FT DOMAIN 95 225 MATH.
FT DOMAIN 265 338 BTB.
SQ SEQUENCE 451 AA; 51062 MW; B36B1C618FBBB3A3 CRC64;

Query Match 30.3%; Score 40; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLP 119
|||||
Db 176 EETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLP 215
|||||

RESULT 15

Q7PRD7
ID Q7PRD7 PRELIMINARY; PRT; 695 AA.

AC Q7PRD7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000013624 (Fragment).
GN Name=ENSANG00000011135;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.

CC EMBL; AAB01008851; EAA07408.2; -
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS0144; MATH; 1.
FT NON TER 695
SQ SEQUENCE 695 AA; 72892 MW; 95934611BB34BDAA CRC64;

Query Match 30.3%; Score 40; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.5e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLP 119
|||||
Db 112 EETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLP 151
|||||

Search completed: July 20, 2005, 20:52:15
Job time : 119.8 secs